

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 18:19:52 ; Search time 8342 Seconds
(without alignments)
11300.779 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175
Sequence: 1 atgtgtaaacgaattatgg.....ataataaagggtggaaaaa 2175

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

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3: gb.in.*

4: gb.ov.*

5: gb.pat.*

6: gb.ph.*

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16: em.fun.*

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18: em.in.*

19: em.mu.*

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40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2175	100.0	2277	1	AF022781	AF022781 Neisseria
2	2175	100.0	2277	6	A98968	A98968 Sequence 1
3	2175	100.0	2277	6	BD074755	BD074755 Neisseria
4	2175	100.0	5691	1	AF049349	AF049349 Neisseria
5	2170.2	99.8	2537	1	AF031432	AF031432 Neisseria
6	1549.8	71.3	2519	1	AF072890	AF072890 Neisseria
7	1487.2	68.4	2226	1	AF123380	AF123380 Neisseria
8	1487.2	68.4	2226	6	A98972	A98972 Sequence 5
9	1487.2	68.4	2226	6	BD074757	BD074757 Neisseria
10	1473	67.7	9955	1	AE002504	AE002504 Neisseria
11	1473	67.7	349980	6	AX044033	AX044033 Sequence
12	1462.2	67.2	2262	1	AF123381	AF123381 Neisseria
13	1462.2	67.2	2262	6	A98974	A98974 Sequence 7
14	1462.2	67.2	2262	6	BD074758	BD074758 Neisseria
15	1454.8	66.9	326301	1	NMA622491	AL162757 Neisseria
16	1304.8	60.0	2169	1	AF123382	AF123382 Neisseria
17	1304.8	60.0	2169	6	A98970	A98970 Sequence 3
18	1304.8	60.0	2169	6	BD074756	BD074756 Neisseria
19	1296.2	59.6	2124	1	AF123383	AF123383 Neisseria
20	1296.2	59.6	2124	6	A98976	A98976 Sequence 9
21	1296.2	59.6	2124	6	BD074759	BD074759 Neisseria
22	678.6	31.2	1000	6	AX081510	AX081510 Sequence
23	678.6	31.2	1000	6	AX374691	AX374691 Sequence
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25	218	10.0	3171	1	NMIRA	X69214 N.meningiti
26	174.2	8.0	3300	1	NGU16260	UI6260 Neisseria g
27	174.2	8.0	3300	6	AX685922	AX685922 Sequence
28	90	4.1	126281	9	HS223H1	AL031943 Human DNA
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33	87.8	4.0	146552	10	AL714007	AL714007 Mouse DNA
34	87.2	4.0	240692	2	AC111246	AC111246 Rattus no
35	87	4.0	181206	2	AC128950	AC128950 Rattus no
36	87	4.0	215429	2	AC128300	AC128300 Rattus no
37	87	4.0	233895	2	AC096447	AC096447 Rattus no
38	86.6	4.0	213739	2	AC113937	AC113937 Mus muscu
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44	85.6	3.9	187930	2	AC124191	AC124191 Mus muscu
45	85.4	3.9	116194	10	BX255946	BX255946 Mouse DNA

ALIGNMENTS

RESULT 1
AF022781
LOCUS AF022781
DEFINITION Neisseria meningitidis lactoferrin binding protein B (1bpB) gene,
complete cds.
ACCESSION AF022781
VERSION AF022781.1 GI:2843172
KEYWORDS
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2277)
AUTHORS Pettersson,A., Prinz,T., Umar,A., van der Biezen,J. and Tommassen,J.

TITLE Molecular characterization of LbpB, the second lactoferrin-binding protein of *Neisseria meningitidis*
JOURNAL Mol. Microbiol. 27 (3), 599-610 (1998)
MEDLINE 94149315
PUBMED 9489671

REFERENCE

AUTHORS 2 (bases 1 to 2277)
Tomassen, J.
Pettersson, A., Prinz, T., Umar, A., van der Biezen, J. and

TITLE Direct Submission
Submitted (04-SEP-1997) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES Location/Qualifiers

source 1..2277

/organism="Neisseria meningitidis"

/mol_type="genomic DNA"

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100..2277

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ORIGIN

Query Match 100.0%; Score 2175; DB 1; Length 2277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCGGCAATTTCGGCGTGCAGCTGTGTGCGATCAACGCGACCGCGTACCGGTCAT 120
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QY 241 CGTGAAGTGGCAGCAATTCGAATACCAACACAGCAGAGAAAGCTGTCGTTCAA 300
DB |||||
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Db 2453 CGCACTCGGGATGACGGCATCGACCTTTCCGGCGAGGTTTCGACCAACCGCAGATCTTC 2512
QY 1921 AAAGCTAATGATCTTTCGTGTAGAGGAGGATTTTACGCCCCGAAAGCGGAGAAATTTGGC 1980
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Db 2633 GTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAA 2692
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Db 2753 AAAGAGGTGGAATAA 2767

RESULT 5
AF031432
LOCUS
DEFINITION
Neisseria meningitidis B16B6 lactoferrin binding protein B
precursor (lbpB) gene, complete cds.
ACCESSION
AF031432
VERSION
AF031432.1
GI:3213214
SOURCE
Neisseria meningitidis
ORGANISM
Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 2537)
Bonnah, R.A. and Schryvers, A.B.
Preparation and characterization of *Neisseria meningitidis* mutants
deficient in production of the human lactoferrin-binding proteins
LbpA and LbpB

JOURNAL

MEDLINE
98292739
PUBMED
9620956

REFERENCE

2 (bases 1 to 2537)

AUTHORS

Bonnah, R.A. and Schryvers, A.B.

TITLE

Direct Submission
Submitted (24-OCT-1997) Microbiology & Infectious Diseases,
University of Calgary, 3330-Hospital Drive N.W., Calgary, AB T2N
4N1, Canada

FEATURES

Location/Qualifiers

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317..335

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360..2537

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360..2537

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360..2534

/product="lactoferrin binding protein B"

ORIGIN

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1441 GCAGGAGATGAGGCGAG 1500
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2340 GGTATTTATTTCAATAATGATGGAATCTCTGTTGTAATGATGATGATGATGATGATGAT 2399
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2520 AAAGAGGTCGAAAA 2534

LOCUS AF072890 2519 bp DNA linear BCT 22-JAN-1999
DEFINITION Neisseria gonorrhoeae lactoferrin binding protein B precursor (lbpB) gene, complete cds.
ACCESSION AF072890
VERSION AF072890.1 GI:4106392
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2519)
AUTHORS Biswas, G.D., Anderson, J.E., Chen, C.J., Cornelissen, C.N. and Sparling, P.F.
TITLE Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product
JOURNAL Infect. Immun. 67 (1), 455-459 (1999)
MEDLINE 99081783
PUBMED 9864256
REFERENCE 2 (bases 1 to 2519)
AUTHORS Biswas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1998) Medicine/D, Univ. of N. Carolina, 521 Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA
FEATURES
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ORIGIN
Query Match 71.3%; Score 1549.8; DB 1; Length 2519;
Best Local Similarity 84.3%; Pred. No. 4.3e-306;

Matches 1874; Conservative 0; Mismatches 262; Indels 87; Gaps 8;

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Dd	427	TTCAAGTCTAAGACGTTCCCACTTTCCCTCCCCCTCGAGCCTTCGCTAGAAACCAAG	486
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Dd	607	AAAGAGGTGATCTCTGTTTTATACGGTTCAAAAGGAAATAACTTCAACCACTTAA	666
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Dd	907	GGCAACTGGCAATATATGACCGATGCAACACGTCATCGACAGGTAAAGCGGTGCGAG	966
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QY	1873	GACGGCATCGACTTTCCGGGAGGGTTCGACCAACCGCAGATCTTCAAGCTAATGAT	1932
Dd	2224	AACGGCATCAATCTTTCCGGGAATGTTTCGATTAATCTTCAAGTTTCAAGCGCAAT	2283
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Dd	2404	GCTGATGTT-----TGCGCAACAGTTAGAACCT	2430


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QY 2113 GAAAGTAAACCCCAATTCGGCGTGGTATTTCGGTGCAGAGAAAGATAATAAAGAGGTGAA 2172
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QY 2173 AAA 2175
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Db 2491 AAA 2493

RESULT 7
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LOCUS Neisseria meningitidis strain H44/76 lactoferrin-binding protein
DEFINITION precursor (lbpB) gene, complete cds.
ACCESSION AF123380
VERSION AF123380.1 GI:4884686
SOURCE
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2226)
AUTHORS Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and
Tomassen,J.
TITLE Sequence variability of the meningococcal lactoferrin-binding
protein lbpB
JOURNAL Gene 231 (1-2), 105-110 (1999)
MEDLINE 99250255
PUBMED 10231574
REFERENCE 2 (bases 1 to 2226)
AUTHORS Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and
Tomassen,J.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES
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ORIGIN
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ACCESSION BD074757
VERSION BD074757.1 GI:22620360
KEYWORDS JP 2001514894-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2226)
AUTHORS Felholm,A.M.P. and Thomassen,J.P.M.
TITLE Neisseria lactoferrin-binding protein

JOURNAL

Patent: JP 2001514894-A 3 18-SEP-2001;
UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION
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PN JP 2001514894-A/3
PD 18-SEP-2001
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THOMASEN
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FH Key Location/Qualifiers

FT source

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Query Match

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ACCESSION			AE002504 AE002098
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ORGANISM			Neisseria meningitidis MC58
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AUTHORS			Neisseriaceae; Neisseria.
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			Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
			Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
			Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
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			Citron, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
			Qin, H., Vanathavan, J., Gill, J., Scarlato, V., Masignani, V.,
			Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
			Rappuoli, R. and Venter, J.C.
			Complete genome sequence of Neisseria meningitidis serogroup B
			strain MC58
			Science 287 (5459), 1809-1815 (2000)
JOURNAL			20175755
MEDLINE			10710307
PUBMED			
REFERENCE			2 (bases 1 to 9955)
AUTHORS			Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
			Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
			Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
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TITLE		Rappuoli, R. and Venter, J.C.
JOURNAL		Direct Submission
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LOCUS
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ACCESSION AX044033
VERSION AX044033.1 GI:11342917
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
Maignani, V., Galeotti, C., Mofa, M., Ratti, G., Scarselli, M.,
Scarlati, V., Rappuoli, R., Frazer, C. M., and Grandi, G.
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 172 09-NOV-2000.
JOURNAL
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
Location/Qualifiers
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RESULT 12
AF123381LOCUS 2262 bp DNA linear BCT 24-MAY-1999
DEFINITION *Neisseria meningitidis* strain m990 lactoferrin-binding protein precursor (lbpB) gene, complete cds.

ACCESSION AF123381

VERSION AF123381.1 GI:4884688

KEYWORDS

SOURCE *Neisseria meningitidis*ORGANISM *Neisseria meningitidis*

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

REFERENCE 1 (bases 1 to 2262)

AUTHORS Petteersen,A., van der Biezen,J., Joosten,V., Hendriksen,J. and

Tomassen,J.

TITLE Sequence variability of the meningococcal lactoferrin-binding protein lbpB
JOURNAL Gene 231 (1-2), 105-110, (1999)
MEDLINE 99250255
PUBMED 10231574
REFERENCE 2 (bases 1 to 2262)
AUTHORS Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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Best Local Similarity 81.1%; Pred. No. 3.4e-288;
Matches 1832; Conservative 0; Mismatches 343; Indels 84; Gaps 8;

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DEFINITION Sequence 7 from Patent WO9909176.
ACCESSION A98974
VERSION A98974.1 GI:6781934
KEYWORDS
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Petterson-Fernholm,A.M. and Tommassen,J.P.
NEISSERIA LACTOFERRIN BINDING PROTEIN
Patent: WO 9909176-A 7 25-FEB-1999;
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ORIGIN

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Query Match 67.2%; Score 1462.2; DB 6; Length 2262;
Best Local Similarity 81.1%; Pred. No. 3.4e-288;
Matches 1832; Conservative 0; Mismatches 343; Indels 84; Gaps 8;
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RESULT 14
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DEFINITION Neisseria lactoferrin-binding protein.
ACCESSION BD074758
VERSION BD074758.1 GI:22620361
KEYWORDS JP 2001514894-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2262)
AUTHORS Felinholm, A.M.P. and Thomassen, J.P.M.
TITLE Neisseria lactoferrin-binding protein
JOURNAL Patent: JP 2001514894-A 4 18-SEP-2001;
UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION
COMMENT OS Unidentified
PN JP 2001514894-A/4
PD 18-SEP-2001
PF 10-AUG-1998 JP 2000009840
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ANICA MARGARETA PETERSON FELINHOLM, JOHANES PETRUS MARIA PI
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CC Topology: Linear;
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LOCUS Neisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION segment 6/7.
ACCESSION AL162757 AL157959
VERSION AL162757.2 GI:7380371
KEYWORDS
SOURCE Neisseria meningitidis Z2491
ORGANISM Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 326301)
AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
Davies,R.M., Davis,P., DeWitt,K., Feltwell,T., Hamlin,N.,
Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,
Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
Skellton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.
TITLE Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491
JOURNAL Nature 404 (6777), 502-506 (2000)
MEDLINE 20222556
PubMed 10761919
REFERENCE 2 (bases 1 to 326301)
AUTHORS Parkhill,J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1BA E-mail: parkhill@sanger.ac.uk
COMMENT Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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Db 17721 TTGCTCAAGATACCTCAACCATCGATCTTCCGACGCGAGAAAATGACCGTCAGTGCT 17662
Qy 1282 TGTTCGCACTTTTTCACCTATGTAAACTCGGACGGATATAAAACCGAACGCCCGCCGCC 1341
Db 17661 TGTTCGCACTTTTTCACCTATGTAAACTCGGACGGATATAAAACCGAACGCCCGCCCAAGT 17602
Qy 1342 AAACCGAAGGCGAGGACGAAGA---GGATTCGGACATTTGATTAATGGCGAAGAAAGCGAA 1398
Db 17601 AAACCAAAAGGCGAAGATGAATAATTCGAGATGAATAATTTGGTGAAGCGAGGAAAAATGAA 17542
Qy 1399 GACGAATCGCGGATGAAGAAGAGGACCGAAGATGACGCGCAGAGAGATGAAGGCGAGC 1458
Db 17541 GAGGATTTGGTCTGCTGAAGAAGAAACACCGAAGACGAAGTCGTAGAAGATGAAGACAGA 17482
Qy 1459 GAAGAAGACGAAGCCACAGAAAAAC----- 1482
Db 17481 GAAGAAGACGAAGTTTCCGAGATGGTTAAACAGTGAAGACGAAGAAATCGCCGAAGAA 17422
Qy 1483 -----GAAAGCGGGAAGAGAGAGAGCTGAAGAACTGTAAGAGAAATCGTCGGCAGAA 1536
Db 17421 GATGATGATGAAGCGAAGAGAGAGAGAGTTGAAGAACCCGGAAGAAATCGCCGGAAGAA 17362
Qy 1537 GGCACAC---GGCAGTTCAAAAGCCATCTGCTGTCCCGGAAGCCTTAAAGGCGAGGAT 1593
Db 17361 GCGCGCGTGGCGGTTCTAGACGGCATCCCGCCGCTTCGGAAGCCCTTAAAGGCGAGGAC 17302
Qy 1594 ATCGACCTTTTCTGAAAGGTATCCGCAACGGAAGAAATATTCGCAAACTGGAGAA 1653
Db 17301 ATCGACCTTTTCTGAAAGGTATCCGCAACGGAAGCGACATTCGCAAACTGGAGAA 17242
Qy 1654 GCACGCTATACCGGCACTTGGGAAGCGGTATCGCAAAACCCATTCATGGGACAAATCAT 1713
Db 17241 GCACGCTATACCGGCACTTGGGAAGCGGTATCAGCAAAACCCATTCATGGGATAATAAG 17182
Qy 1714 GCGGATGAAGAGCGCAAAACGACGATTTACCGTTGATTTCCGCAAGAAATCGATTTCC 1773
Db 17181 GCGGATGAAGAGCGCGCAAAACGAGATTTGACGTTGATTTCCGCGAGAAATCGATTTCC 17122
Qy 1774 GGAACGCTGACGGAGAAAAACGGTGTAGAACCTGCTTTCCGTATTTGAAAAACGGGTGATT 1833
Db 17121 GGAACGCTGACGGAGAAAAACGGTGTAGAACCTGCTTTCTATATTTGAAAAAGGTGTGATT 17062
Qy 1834 GAGGGCAACGGTTTCATGCGACAGGCGCATCGGATCAGGCATCGACCTTTCCGGG 1893
Db 17061 GATGGCAACGGTTTCCACGCGACGACGCACTCGGATTAACGGCATCAATCTTTCCGGGA 17002
Qy 1894 CAGGGTTCCACCAACCGCAGATCTTCAAGCTAATGATCTTCGTGTAGAGGAGATT 1953
Db 17001 AATGGTTCCACCAACCCCAAAACCTTCCAAGCTAGTATCTTCGTGTAGAGGAGATT 16942
Qy 1954 TACGGCCCGAAGCGGAGGAATTTGGCGGTATTTATTTTCAATAATGATGGGAAATCTCTT 2013
Db 16941 TACGGCCCGCAGCGGAGGAATTTGGCGGTACTATTTTCAATAAGATGGGAAATCTCTT 16882
Qy 2014 GGTATAACTGAAGGTACTGAATAAAGTTGAAGCTGATGTTGATGTTGATGTT 2073
Db 16881 GATATAACTGAAGATATTGACAAATGAAATTTGAAGCTGA----- 16844
Qy 2074 GATGTTGATGCTGATGCTGATGTTGACAGTGTAAACCTTGAAGTTAAACCCCAATTCGGC 2133

Db 16843 -----TGCTGGCGAACAGTTAGAACCTGAAGTTAAACCCCAATTCGGC 16801
Qy 2134 GTGGTATTCGGTCCGGAAGAAAGATAATAAAGAGGTGGAAAA 2175
Db 16800 GTGGTATTTGGTGGCAAAAAAGATATCGAGAGGTGGAAAA 16759

Search completed: August 23, 2004, 22:06:13
Job time : 8360 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 16:54:52 ; Search time 835 Seconds

(without alignments)
11065.666 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175

Sequence: 1 atgtgtaaacgaattatgg.....ataataaagaggtaggaaaaa 2175

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_29Jan04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2175	100.0	2277	2	AAX23319 N. mening
2	1487.2	68.4	2226	2	AAX23321 N. mening
3	1473	67.7	110000	3	Continuation (2 of
4	1473	67.7	349980	3	AAX21611 Neisseria
5	1462.2	67.2	2262	2	AAX23322 N. mening
6	1454.8	66.9	2226	7	ACA41945 Prokaryot
7	1304.8	60.0	2169	2	AAX23320 N. mening
8	1296.2	59.6	2124	2	AAX23323 N. mening
9	1010.4	46.5	14652	3	AAA81482 N. mening
10	678.6	31.2	1000	6	AAF91389 N. mening
11	678.6	31.2	1000	6	ABK37769 DNA seque
12	460.4	21.2	707	3	AAA81815 N. mening
13	174.2	8.0	3300	6	ABS67377 Neisseria
14	88.2	4.1	2139	2	AAX231947 M. catarr
15	81.2	3.7	801	5	AAS90729 DNA encod
16	80.8	3.7	510	5	AAS90687 DNA encod
17	80.8	3.7	510	5	AAS69539 DNA encod
18	80.8	3.7	510	5	AAS71141 DNA encod
19	79.4	3.7	54786	8	ADA02705 Mouse zfh
20	79.4	3.7	54786	9	ADB72443 Mouse zfh
21	79	3.6	379	5	AAS90909 DNA encod
22	79	3.6	379	5	AAS75428 DNA encod
23	79	3.6	379	9	AD809716 Novel DNA

24	79	3.6	2114	2	AAT11242	Aat11242 Neisseria
25	78	3.6	248	5	AAS90707	Aas90707 DNA encod
26	78	3.6	305	4	AAI21797	Aai21797 Probe #11
27	78	3.6	305	4	ABA66871	AbA66871 Human foe
28	78	3.6	305	4	AAI47083	Aai47083 Probe #15
29	78	3.6	305	4	ABA48950	AbA48950 Human bre
30	78	3.6	305	4	ABA33942	AbA33942 Probe #12
31	78	3.6	305	4	AAK41027	Aak41027 Human bon
32	78	3.6	305	4	AAK15306	Aak15306 Human bra
33	78	3.6	305	4	ABS40624	AbS40624 Human liv
34	78	3.6	305	5	AAI07480	Aai07480 Probe #74
35	78	3.6	305	6	ABS15007	AbS15007 Human gen
36	78	3.6	400	5	AAS75460	Aas75460 DNA encod
37	78	3.6	483	5	AAS69549	Aas69549 DNA encod
38	78	3.6	496	4	AAI12609	Aai12609 Probe #25
39	78	3.6	496	4	ABA54309	AbA54309 Human foe
40	78	3.6	496	4	AAI33960	Aai33960 Probe #26
41	78	3.6	496	4	ABA43847	AbA43847 Human bre
42	78	3.6	496	4	ABA24068	AbA24068 Probe #25
43	78	3.6	496	4	AAK28026	Aak28026 Human bon
44	78	3.6	496	4	AAK02592	Aak02592 Human bra
45	78	3.6	496	4	ABS27626	AbS27626 Human liv

ALIGNMENTS

RESULT 1
AAX23319
ID AAX23319 standard; cDNA; 2277 BP.
XX
AC AAX23319;
XX
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain BNCV LbpB cDNA.
XX
LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT CDS 100..2277
FT /*tag= a
FT /*product= "LbpB"
XX
PN WO9909176-A1.
XX
PD 25-FEB-1999.
XX
PF 10-AUG-1998; 98WO-EP005117.
XX
PR 15-AUG-1997; 97GB-00017423.
XX
PR 05-FEB-1998; 98GB-00002544.
XX
(UYUT-) RIJKSUNIV UTRECHT.
XX
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESRICHTING ST.
XX
Petterson-Fernholm AM, Tommassen JPM;
XX
WPI: 1999-190165/16.
XX
P-PSDB; AAW93492.

New lactoferrin-binding protein B polynucleotides - obtained from Neisseria meningitidis, used to develop products for the diagnosis, prevention and treatment of neisserial disease, e.g. meningitis.

Claim 2; Page 74-78; 116pp; English.

This invention describes novel lactoferrin-binding protein B (LbpB) strains of Neisseria meningitidis. The products of this invention can be used for vaccinating humans against neisserial disease e.g. meningitis.

CC Antibodies raised against the proteins of the invention can be used for
CC diagnosing or treating neisserial disease in humans. The lbpB
CC polypeptides can also be used for identifying compounds which inhibit the
CC polypeptides

XX Sequence 2277 BP; 700 A; 469 C; 573 G; 535 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 2175; DB 2; Length 2277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTAACCGGAATATGCGGCAATGTCTGTGTCGACCTTCAACGCGCGACCGGTACCCGTCACCT 120
DB 100 ATGTGTAACCGGAATATGCGGCAATGTCTGTGTCGACCTTCAACGCGCGACCGGTACCCGTCACCT 159
QY 61 GCGGCGCAATTTCCGCGTGCAGCCTTGTGTCGAATCAACGCGCGACCGGTACCCGTCACCT 120
DB 160 GCGGCGCAATTTCCGCGTGCAGCCTTGTGTCGAATCAACGCGCGACCGGTACCCGTCACCT 219
QY 121 TTCAGGTCTAAGACCGTTCCTCACTCCGCCCCCTGCCAAACCTTCTATAGAAATCACGCGG 180
DB 220 TTCAGGTCTAAGACCGTTCCTCACTCCGCCCCCTGCCAAACCTTCTATAGAAATCACGCGG 279
QY 181 GTCAACGCGCCCGCTCGGTGCGGCAATGCGGCTGCGAAGCGGCGAATACGTCTTTCAT 240
DB 280 GTCAACGCGCCCGCTCGGTGCGGCAATGCGGCTGCGAAGCGGCGAATACGTCTTTCAT 339
QY 241 CGTGAAGATGGCAACGGAATTTCCAAATAGCAAAACAAAGCAAGCAAGAAAGCTGTCGTTTCAA 300
DB 340 CGTGAAGATGGCAACGGAATTTCCAAATAGCAAAACAAAGCAAGCAAGAAAGCTGTCGTTTCAA 399
QY 301 GAAGGTGATGTTCTGTTTTATACCGTTCAAAAGGAAATAAACTTCAACAACTTAAAGC 360
DB 400 GAAGGTGATGTTCTGTTTTATACCGTTTCAAAAGGAAATAAACTTCAACAACTTAAAGC 459
QY 361 GAATTCATAAAGCGTTCGATGTCGATGTAGAAATTTAGACATCAGAAAGGAAATATAAAA 420
DB 460 GAATTCATAAAGCGTGAATTCGATGTAGAAATTTAGACATCAGAAAGGAAATATAAAA 519
QY 421 TATGATTATAAAATTCTGATGATGAGGTATGATATATGTAAGGAAAGATGAAATTAAG 480
DB 520 TATGATTATAAAATTCTGATGATGAGGTATGATATATGTAAGGAAAGATGAAATTAAG 579
QY 481 TGGACTTCAGATTACAGCAGTTTCCAAACCGTTAGGTATGACGTTTGTATATAT 540
DB 580 TGGACTTCAGATTACAGCAGTTTCCAAACCGTTAGGTATGACGTTTGTATATAT 639
QY 541 TCCGAGAGACGTCCTTCCCAATCTTTACCGAGTGCAGGACCGTGGAAATATCTGCTAAC 600
DB 640 TCCGAGAGACGTCCTTCCCAATCTTTACCGAGTGCAGGACCGTGGAAATATCTGCTAAC 699
QY 601 TGGCAATATATGACCGATGCAAAACGTCATCGAGCAGGTAAGCGGTTGGCAATTGACAAT 660
DB 700 TGGCAATATATGACCGATGCAAAACGTCATCGAGCAGGTAAGCGGTTGGCAATTGACAAT 759
QY 661 TTGGGTTATTAACATTTTATGTTAAGATGATGTTGTCGAACTTCTTATCGGCTAAGGAT 720
DB 760 TTGGGTTATTAACATTTTATGTTAAGATGATGTTGTCGAACTTCTTATCGGCTAAGGAT 819
QY 721 GTCGACGAAGGGAACCAATCTGCTAAATATACGTTAGATTTCCGTAACAAACCCCTG 780
DB 820 GTCGACGAAGGGAACCAATCTGCTAAATATACGTTAGATTTCCGTAACAAACCCCTG 879
QY 781 ACGGCGAGCTGATTATAAACCAATATGTCAACCCAGTGAGAGCAAAAACCGCTGACC 840
DB 880 ACGGCGAGCTGATTATAAACCAATATGTCAACCCAGTGAGAGCAAAAACCGCTGACC 939
QY 841 ATTTACAAATCATCTCCCGATTTAACGCGCAACCGCTTTACCGGCGAGTCCAGGTCAAT 900
DB 940 ATTTACAAATCATCTCCCGATTTAACGCGCAACCGCTTTACCGGCGAGTCCAGGTCAAT 999
QY 901 CCTGATTTAGCAAAAAGCCATGCCAATAAGGACATTTGTTTTTCCATGCCGATGCCGAT 960

DB 1000 CCTGATTTAGCAAAAAGCCATGCGCAATAGGAGCAATTTGTTTTTCCATGCCGATGCCGAT 1059
QY 961 CAGCGGCTTCAGGCGGCTTTTTTCGGCGATAAGGGGGAAGAGCTTTCGGGACGTTTATC 1020
DB 1060 CAGCGGCTTCAGGCGGCTTTTTTCGGCGATAAGGGGGAAGAGCTTTCGGGACGTTTATC 1119
QY 1021 AGCAACGACAAACAGCGGTATTCGGTGTATTCGCGAGGCAAAACAAATATGCCCGTCCGCTCT 1080
DB 1120 AGCAACGACAAACAGCGGTATTCGGTGTATTCGCGAGGCAAAACAAATATGCCCGTCCGCTCT 1179
QY 1081 GGAACACACACCAAAATCTTGGATTCTCTGAAATATTCCTGATGAGGCAAGTGTGAA 1140
DB 1180 GGAACACACACCAAAATCTTGGATTCTCTGAAATATTCCTGATGAGGCAAGTGTGAA 1239
QY 1141 AATCCCGACCGCTTTCGCAATTTCTCTATGCCGATTTTGTGTCATCCGCAAACTTCTT 1200
DB 1240 AATCCCGACCGCTTTCGCAATTTCTCTATGCCGATTTTGTGTCATCCGCAAACTTCTT 1299
QY 1201 GTCGAAAGGCGATGAAATTCCTTTGTTAGCAAGAGAAACCATTCGAGCTTTCGCAAGC 1260
DB 1300 GTCGAAAGGCGATGAAATTCCTTTGTTAGCAAGAGAAACCATTCGAGCTTTCGCAAGC 1359
QY 1261 AGGAAATGACCTCAGTGTCTTGGACCTTTTGAACCTATGTGAAACTCGGACGATGATA 1320
DB 1360 AGGAAATGACCTCAGTGTCTTGGACCTTTTGAACCTATGTGAAACTCGGACGATGATA 1419
QY 1321 AAAACCGAACCGCCCGCCGCAACCGAAGCGCAGGACGAGAGGATTCGGACATTTGAT 1380
DB 1420 AAAACCGAACCGCCCGCCGCAACCGAAGCGCAGGACGAGAGGATTCGGACATTTGAT 1479
QY 1381 AATGGCGAAGAAAGCGAAGACGAAATTCGGCGATGAAAGAAAGGACCCGAGATTCGAGCC 1440
DB 1480 AATGGCGAAGAAAGCGAAGACGAAATTCGGCGATGAAAGAAAGGACCCGAGATTCGAGCC 1539
QY 1441 CGAGGAGATGAGGCGAGCGAAGAGAGAGACGACAGAGCCACAGAAACGAGCGGAGAGAC 1500
DB 1540 GCAGGAGATGAGGCGAGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1599
QY 1501 GAAGCTGAAGAACCTCAAGAAAGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1600 GAAGCTGAAGAACCTCAAGAAAGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1659
QY 1561 CTGCTGTCTCCGGAAGCCTTAAAGCGAGGATATCGACCTTTCTCTGAAAGGATTCGCG 1620
DB 1660 CTGCTGTCTCCGGAAGCCTTAAAGCGAGGATATCGACCTTTCTCTGAAAGGATTCGCG 1719
QY 1621 ACGGCGAAGAACGATATTCGCAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1720 ACGGCGAAGAACGATATTCGCAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1779
QY 1681 CGTATCGCAAAACCCATTCATGGGCAATCATGCGGATAAAGAAAGCGGCAAAAGCAGTA 1740
DB 1780 CGTATCGGCAAAACCCATTCATGGGCAATCATGCGGATAAAGAAAGCGGCAAAAGCAGTA 1839
QY 1741 TTATCGGTTGATTTCCGCAAGAAATCGATTTCCGGAACGCTGACGAGAGAAACCGGTGTA 1800
DB 1840 TTATCGGTTGATTTCCGCAAGAAATCGATTTCCGGAACGCTGACGAGAGAAACCGGTGTA 1899
QY 1801 GAACCTGCTTCCGTTATGAAACCGGCTGATTTGGGCAACGCTTCCATGCGACAGCG 1860
DB 1900 GAACCTGCTTCCGTTATGAAACCGGCTGATTTGGGCAACGCTTCCATGCGACAGCG 1959
QY 1861 CGCACTCGGATGACGCGCATCGACCTTTCCGCGGAGGTTTCGACCAAAACCGCAGATCTTTC 1920
DB 1960 CGCACTCGGATGACGCGCATCGACCTTTCCGCGGAGGTTTCGACCAAAACCGCAGATCTTTC 2019
QY 1921 AAGCTAATGATCTTCGTGTAGAGAGGATTTACGCGCCCGAAGCGGAGGATTTGGG 1980
DB 2020 AAGCTAATGATCTTCGTGTAGAGAGGATTTTACGCGCCCGAAGCGGAGGATTTGGG 2079
QY 1981 GGTATTTATTTTCAATAATGATGGAATCTCTTGGTATTAACCTGAAGTACTGAAATATAA 2040
DB 2080 GGTATTTATTTTCAATAATGATGGAATCTCTTGGTATTAACCTGAAGTACTGAAATATAA 2139

1099 TTGGATTCTCTGAAATTTTCGGTTGATGAGCGAAGTGTGAAATCCCGACCGTTTGCC 1158
Db |||||
1141 TTGGATTCTCTGAAATTTTCGGTTGATGAGCGAAGTGTGAAATCCCGACCGTTTGCC 1200
Qy |||||
1159 ATTCTCTATGCCCGATTTTGGTCAATCCCGACAAATCTTCTGTCGAAGGCGATGAAT 1218
Db |||||
1201 ATTTCCTCTGCGCGATTTTGGCCATCCCGACAAATCTCTTGTGCGAAGGCGTGAAT 1260
Qy |||||
1219 CTTTGGTTAGCCAGAAACCATCGAGTTGCCAGCGCAGGAGAAATGACCGTCAGT 1278
Db |||||
1261 CTTTGGTTAGCCAGAAACCATCGAGTTGCCAGCGCAGGAGAAATGACCGTCCT 1320
Qy |||||
1279 GCTTGTTCGACATTTTGTGACTATGTGAATCTCGACGCGATATAAACCAGCGCCGCC 1338
Db |||||
1321 GCTTGTTCGACTTTTCTGACTATGTGAATCTCGACGCGATATAAACCAGCGCCAGCA 1380
Qy |||||
1339 GCCAAACCGAAGG-----GCAGACGAAGAGATTTCGACATGATATATGCG 1386
Db |||||
1381 AGTAAACCAAGCGGAAGATAAAGGGAAGGATGAAGAGGATACAGCGTTGTTAACGAC 1440
Qy |||||
1387 GAAGAAAGC---GAAGACGAATCGCGATGAAGAGGACCGAAGATGCGACCGCA 1443
Db |||||
1441 GAAGAGCGACGGAATGAGCGCGAAGAGCGAGCGAAGGCGGAAGCGGAATCGCG 1500
Qy |||||
1444 GAGATGAAGCGCAGCAAGAGACGAGCCACAGAAACCAAGACCGCGCAAGAGAGCA 1503
Db |||||
1501 GATGAAGGAGGAGTTCGGAAGACGAGCGCAGAGAAACGAGCGCGCAAGAGAGCA 1560
Qy |||||
1504 GCTGAAGAACCT-----GAAGAGAAATCGTTCGCGAAGGCAAC---GGAGTTCA 1551
Db |||||
1561 GCTGAAGAACCTGAAGAACCGAAGAGAGAAATCGCGCGAAGCGCGGTGTGTTCA 1620
Qy |||||
1552 AAGCCATCTGCTGTCGCGAAGCCTTAAGGCGAGGATACGACCTTTTCCGTAAA 1611
Db |||||
1621 GACGGATCTGCGCGTCCGGAAGCTCTTAAGGCGAGGATACGACCTTTTCCGTAAA 1680
Qy |||||
1612 GGTATCGCACGCGCAAGAAACCAATATTCGCAAACTGGAGAAGCACGCTATACCGGCACT 1671
Db |||||
1681 GGTATCGCACGCGCAAGCGGACATTCGCAAACTGGAGAAGCACGCTATACCGGCACT 1740
Qy |||||
1672 TGGGAAGCGGTATCGGCAAAACCAATTCATGGAGCAATCATCGGATATAAGAGCGCA 1731
Db |||||
1741 TGGGAAGCGGTATACGCAAAACCAATTCATGGAGCAATCATCGGATATAAGAGCGCA 1800
Qy |||||
1732 AAAGCAGTATTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAACGCTGACGAGAA 1791
Db |||||
1801 AAAGCAGTATTTGACGTTGATTTCCGCGAAGAAATCGATTTCCGGAACGCTGACGAGAA 1860
Qy |||||
1792 AACGGTGTAGAACTGCTTTCCGTATTTGAAACCGGCGTGATTTAGGGCAACGCTTTCCAT 1851
Db |||||
1861 AACGGTGTACAACTGCTTTCCATATTTGAAACCGGCGTGATTTAGGGCAATGTTTCCAC 1920
Qy |||||
1852 GCGACAGCGGCACTCGGATGACGCGATCGACCTTTCCGCGCAGGTTTCGACCAACCG 1911
Db |||||
1921 GCGACAGCGGCACTCGGATGACGCGATCAATCTTTCCGGAATGATTCGACCAATCTCT 1980
Qy |||||
1912 CAGATCTTCAAGCTTAATGATCTTCGTGTAGAGAGGATTTTACGCGCGAGGCGGAG 1971
Db |||||
1981 CCAAGTTTCAAGCCAAATATCTTTGTAACAGGCGGCTTTTACGCGCGAGGCGGAG 2040
Qy |||||
1972 GAATTGGCGGATATTTTCAATAATGATGGGAAATCTCTTGGTATACTGAAGGTACT 2031
Db |||||
2041 GAATTGGCGGATATTTTCAATAATGATGGGAAATCTCTTGGTATACTGAAGGTACT 2100
Qy |||||
2032 GAATAAAGTTCAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2091
Db |||||
2101 GAATAAAGTTCAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2141
Qy |||||
2092 GATGTTGAAACAGTTAAACCTGAAGTTAAACCCCAATTCGGCGTGTGTTTCGGTGGAG 2151
Db |||||
2142 --TGGCGAAGTTAAACCTGAAGTTAAACCCCAATTCGGCGTGTGTTTCGGTGGAG 2199

2152 AAAGATAATAAGAGGTGGAATA 2175
Db |||||
2200 AAAGATAATAAGAGGTGGAATA 2223
Qy |||||
RESULT 3
AA81489 1/c
Continuation (2 of 9) of AA81489 from base 100001 (N. meningitidis partial DNA sequenc
WP Sequence split into 9 fragments LOCUS AA81489 Accession AA81489
WP Fragment Name Begin End
WP AA81489_0 1 110000
WP AA81489_1 100001 210000
WP AA81489_2 200001 310000
WP AA81489_3 300001 410000
WP AA81489_4 400001 510000
WP AA81489_5 500001 610000
WP AA81489_6 600001 710000
WP AA81489_7 700001 810000
WP AA81489_8 800001 837096
Query Match 67.7%; Score 1473; DB 3; Length 110000;
Best Local Similarity 81.9%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches 310; Indels 96; Gaps 8;
Qy 1 ATGTGTAACCGGAATATATGCGGCAATGTCTTGTGCCCCTTACTTTTGGCATCTTGTATC 60
Db 64252 ATGTGTAACCGGAATATATGCGGCAATGTCTTGTGCCCCTTACTTTTGGCATCTTGTATC 64193
Qy 61 GCGGCAATTTTCGGGTGACGCTTGTTCGAATCAACGCGCACCGGTTACCGGTCAC 120
Db 64192 GCGGCAATTTTCGGGTGACGCTTGTTCGAATCAACGCGCACCGGTTACCGGTCAC 64133
Qy 121 TTCAAGTCTAAGACGCTTCCCACTCCGCCCTTGCACAACTTCTATAGAAATCAACGCG 180
Db 64132 TTCAAGTCTAAGACGCTTCCCACTCCGCCCTTGCACAACTTCTATAGAAATCAACGCG 64073
Qy 181 GTCAACGCGGCCCGCTCGGTGCGCAATTCGGCTGCCAAGGCGGAATATCTGCTTTTCAT 240
Db 64072 GTCAACGCGGCCCGCTCGGTGCGCAATTCGGCTGCCAAGGCGGAATATCTGCTTTTCAT 64013
Qy 241 CGTGAAGATGCGACGGAATTTCCAAATAGCAAAACAGCAGAGAAAGCTGTGCTTTCAA 300
Db 64012 AAACAAGACGCTACGGAATTTCCCGACAGCATCAGCAGAGGAGCATCTGCCGCTTAAA 63953
Qy 301 GAAGGTGATCTTCTGTTTATACGTTTCAAAAGGAAATAAATCTCAACACTTAAAGC 360
Db 63952 GAGAAGATATCTGTTTTTAGACGGTACGCTGAAAGAACGCGTGACAAACTTTAAAG 63893
Qy 361 GAAATTCATAAACGTCGATTCGGATAGAAATTAGGACATCAGAAAGGAAATAAAAA 420
Db 63892 AAAATCAACGACGCTATCTGATGTGAGGTTTATCACATCGAAAGAGAGAGAA 63833
Qy 421 TATGATTTAAATTTGTAGATGACGTTATGTATGTATGTAAAGGAAAG-----AT 471
Db 63832 TATCAATATCAATTTTGTGCGGTATGTGTTTACCAGGCGGAAAGAGGATAAT 63773
Qy 472 GAAATTAAGTGGACTTTCAGATTAACAAGCAGTTTTCACACCGCTTAGTATGACGTTTT 531
Db 63772 GAAAAAGAAAGACTTCTGATGTAAAGGTTTGTAAACGATTTAGTTATGACGTTTT 63713
Qy 532 GTATATTTTCCGGAGAACGCTCTTCCCAATCTTTTACCAGAGTCCGGGAAACGTTGAAAT 591
Db 63712 GTATATTTTCCGGAGAACGCTCTTCCCAATCTTTTACCAGAGTCCGGGAAACGTTGAAAT 63653
Qy 592 TCTGGTAACTGGCAATATATGACCGATGCAACAGTCTATCGACAGGTAAAGCGGTTGGC 651
Db 63652 TCCGGTAACTGGCAATATATGACCGATGCAACAGTCTATCGACAGGTAAAGCGGTTTC 63593
Qy 652 ATTGACAAATTGGGTTATTACATTTTATGGTAAACGATGTTTGGTCAACTCTTTATGCG 711
Db 63592 AGTACGGATTTGGGTTATTACCAATATATGTTATGTAATGGGCAACTCTTTATGAG 63533
Qy 712 GCTAAGGATGTGCAAGAAAGGGAACATCTCTGCTAAATATATACGTTAGATTTTCGGTAAC 771

CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 4980 bp
 CC (i.e. the last 4980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 4980 bp of AAF21607 are repeated at the beginning of
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting infection due to Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used
 XX
 SQ Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;

Query Match 67.7%; Score 1473; DB 3; Length 349980;
 Best Local Similarity 81.3%; Pred. No. 0;
 Matches 1835; Conservative 0; Mismatches 310; Indels 96; Gaps 8;

QY 1 ATGTGTAACCGGAATATGCGGCATGTCTTGTCCTTACCTTTGGCATCTTGATC 60
 DB 99481 ATGTGTAACCGGAATATGCGGCATGTCTTGTCCTTACCTTTGGCATCTTGATC 99422

QY 61 GCGCGCAATTCGGGTGAGCTGTGTGCGAATCAACGCGCAGCGGTACCCCGTCACT 120
 DB 99421 GCGCGCAATTCGGGTGAGCTGTGTGCGAATCAACGCGCAGCGGTACCCCGTCACT 99362

QY 121 TTCAAAGCTAAGACGTTCCCATCCGCGCCCTCCGCAACCTTCTATAGAAATCAAGCGG 180
 DB 99361 TTCAAATCTAAGACGTTCCCATCCGCGCCCTCCGCAACCTTCTATAGAAATCAAGCGG 99302

QY 181 GTCAACCGGCGCCCGTGGTGGCGCAATGCGGCTGCAAGGCGGAATCTGCTTTTCAT 240
 DB 99301 GTCAACCGGCGCCCGTGGTGGCGCAATGCGGCTGCAAGGCGGAATCTGCTTTTCAT 99242

QY 241 CGTGAAGATGGCAGAAATTCAAATAGCAAAACAAAGCGAAGAAAGCTGTGCTTCAA 300
 DB 99241 AAACAAGCGGTACGGAAATTCGCGCAAGCATCAGGCGAGAGCATCTGCGCTTAA 99182

QY 301 GAAGGTGATGTTCTGTTTTATACGTTTCAAAGGAAATAAATCTCAACAACTTAAAGC 360
 DB 99181 GAGAAGGATATCTGTTTTTAGCGTACGCTGAAGAACAGGCTGACAACTTAAAG 99122

QY 361 GAAATTCATAAACGATTCGATGTAGAAATTTAGGACATCAGAAAGGAAATAAAAA 420
 DB 99121 AAAATCAACGAACGGTATCTGATGTGAGGGTTATCACAATCGAAAGAAAGAGAA 99062

QY 421 TATGATTATAATTTCTAGATCGAGTTATGTATATGTAAAGGAAAG-----AT 471
 DB 99061 TATCAATATCAATTTGTCGTCGGGCTATGTGTTTACAGGCGGAGAAAGGATAAT 99002

QY 472 GAAATTAAGTGACTTCAGATTACAGCAGTTTCCAAACCGCTTAGGTTATGACGGTTTT 531
 DB 99001 GAAAGAAGAAAGACTTCTGATGGTAAGAGTTTGTATACCGAATTAGTTATGACGGTTTT 98942

QY 532 GTATATTAATTCGGGAAGCTCTTCCCAATCTTTACCGAGTCCGGGAACGGTGAATAT 591
 DB 98941 GTATATTAATTCGGGAAGCTCTTCCCAATCTTTACCGAGCGCGGAACGGTGAATAT 98882

QY 592 TCTGGTAACTGCAATATATGACCATGCAACGCTCATCGAGCAGGTGAAGCGGTGGC 651
 DB 98881 TCCGGTAACTGCAATATATGACCATGCAACGCTCATCGAGCAGGTGAAGCGGTGGC 98822

QY 652 ATTGAACAATTTGGTTATPACACATTTATGTTAAGATGTTGGTGCACTTCTTATGCG 711
 DB 98821 ACTACGGATTGGTTATACCAATATATGTTAAGATGTTGGTGCACTTCTTATGAG 98762

QY 712 GCTAAGGATGTGACGAAGGGAACATCTCTCTAAATATACGTTAGATTTCGGTAAC 771
 DB 98761 GCTAAGGATGCCGACGACAGGAAAGCATCTCTCCGAATATACGGTTGTTGATAAC 98702

QY 772 AAAACCTTGACGGCGAGCTGATTAAAAAACCAATATGT-----CAAAACCCAGT 819
 DB 98701 AAAACCTGATGCGAAGCTGATTAAAAATCAGTATGTGCAAAATAAAGTAATCCAAAT 98642

QY 820 GAGAAGCAAAAACCGCTGACATTTACAAATCATCATCTCCGATTTTAAACGCAACCGCTTT 879
 DB 98641 GAGCCCAAAAACCGCTGACATTTACGACATACCGCAACATTTGAGCGGCAACCGCTTT 98582

QY 880 ACCGGCAGTCCCAAGGTCAATCTGTATTAGCGAAAGCCATGCCAATTAAGGACATTG 939
 DB 98581 ACCGGCAGTCCCAAGGTAGCACCGAGGTGAAGACGCAACACGCTGATAAAGAAATATTG 98522

QY 940 TTTTTCATGCGGATGCGGCTTTCAGCGGCTTTGAGGGCGGTTTTTTTCGCGGATTAAGGGGAA 999
 DB 98521 TTTTTCATGCGGATGCGGCTTTCAGCGGCTTTGAGGGCGGTTTTTTTCGCGGATTAAGGGGAA 98462

QY 1000 GAGCTTCCCGGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGTATTTCCGAGGCAAA 1059
 DB 98461 GAGCTTCCCGGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGTATTTCCGAGGCAAA 98402

QY 1060 CAAAAATA-----GCCCCGTGCGCTCTGGAACAC 1089
 DB 98401 CAAAAACAGACAGACAGAAACGCGACGATACAAAACCTCCCTGTCTGTGGAACAC 98342

QY 1090 ACCAAATCTTGATTTCTCTGAAAAATTTCCGTTGATGAGCAAGTGTGAAAAATCCCGGA 1149
 DB 98341 ACCAAATCTTGATTTCTCTGAAAAATTTCCGTTGATGAGCAAGTGTGAAAAATCCCGGT 98282

QY 1150 CCGTTTGCAATTTCTCTATGCCGATTTTGTCTATCCCGAACAATCTTCTGTGCAAGGG 1209
 DB 98281 GAGTTTGCAATTTCTCTATGCCGATTTTGTCTATCCCGAACAATCTTCTGTGCAAGGG 98222

QY 1210 CATGAAATTCCTTTGTTAGCAGAAAGAAACCATCGAGCTTCCGACGCGCGCAAAATG 1269
 DB 98221 CGTGAATTTCTTTTGTAAACAAAGAAACAAACATCGAGTTGCCGATGTGAGAAACG 98162

QY 1270 ACCGTGAGTGTGTTTTCGATTTTGTGACCTATGTGAAATCTCGGACGGATATAAAACCGAA 1329
 DB 98161 ACAATCCGAACTGTGCGATTTTCTGACCTATGTGAAATCTCGACGGATGCAACCGAA 98102

QY 1330 CGCCCCCGCCCAACCGGAGGGCGAGGACGAGAG-----GATTGCGACATT 1377
 DB 98101 CGTCCCGCCCAACCGGAGGGCGAGGACGAGAGGAGGACGAGAGGATACAGCGGTT 98042

QY 1378 GATAATGGCGAAGAAAGCAAGCAAGAAATCGGCGATGAAGAGAGGACCGAAGATGCA 1437
 DB 98041 GATAGCTCGAAGAGGCGAAGCAAGAAATCGAGAT---GAAGAGGACCGGAGACGCA 97985

QY 1438 GCGCAGGAGATGAAGGCGAGCAAGAAAGCAAGCGCACAGAAACGAGACGCGCAAGAA 1497
 DB 97984 GCGCTAAAAGACGAAAGCAGCAAGAAAGCAAGCGCGTAGAA-----GCTGAA 97937

QY 1498 GACGAGCTGAAGACCTTGAAGAGATCGTCG---GCAAGGCGAAACGCGAGTTCAAAC 1554
 DB 97936 GATGAAGCTGAAGAACCCGAGAGAAATCCCGACAGAAAGAGGCGGCGGTTTCAGAC 97877

QY 1555 GCCATCTGCTGTCCCGGAAGCCCTTAAAGGCGAGGATATCGACTTTTCTTGAAGGT 1614
 DB 97876 GCCATCTGCTGTCCCGGAAGCCCTTAAAGGCGAGAAATCGACTTTTCTTGAAGGT 97817

QY 1615 ATCCGACGCGAAGAAAGAAATTCGCAAACTGGAGAGACGCTATATACCGCACTTG 1674
 DB 97816 ATCCGACGCGAAGAAAGGATATTCGAAAACTGGAGAGACACATATATACCGCACTTG 97757

QY 1675 GAAGCGGTATCGGCAACCCCAATTCATGGGCAATCATGCGGATTAAGAAAGCGGCAAAA 1734
 DB 97756 GAAGCGGTATCGGCAACCCCAATTCATGGGCAATCATGCGGCGGATTAAGAAAGCGGCAAAA 97697

[illegible]

RESULT 5

RESULTS 3
AAX23322
ID AAX23322 standard; cDNA; 2262 BP.

AC AAX23322;

DT 11-JUN-1999 (first entry)

DE N. meningitidis strain M990 LbpB cDNA.

XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis: diagnosis; treatment; ds.
KW

Neisseria meningitidis.

XX	Key	Location/Qualifiers
FH	CDS	1. .2262
FT		

W09909176-A1

XX
PD
25-FEB-1999

XX
DE 10-2117-1000. 99WC-EP005117

XX

PR 05-FEB-1998; 98GB-00002544.

PA (UYUT-) RIJKSUNIV UTRECHT.
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

PI Pettersson-Fernholm AM, Tommassen JPM;

AA WPI: 1999-190165/16.

DR WFI; I999-I901837
DR P-PSDB; AAW93495.

XX New lactoferrin-binding protein B polynucleotides - obtained from
PT
PT Neisseria meningitidis, used to develop products for the diagnosis,
PT prevention and treatment of neisserial disease, e.g. meningitis.

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;

Query Match 66.9%; Score 1454.8; DB 7; Length 2226;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 1839; Conservative 0; Mismatches 297; Indels 126; Gaps 8;

Qy	1	ATGTGTAACCGAATTATGGGGCAATTCCTGTGTGTCCTTACTTTTGGCATCTTGATC	60
Db	1	ATGTGTAACCGAATTATGGGGCAATTCCTGTGTGTCCTTACTTTTGGCATCTTGATC	60
Qy	61	GGCGCAATTTCCGGGTGCGAGCTGTGTCGAATCAACGCCGACCGCGTACCCGTCAC	120
Db	61	GGCGCAATTTCCGGGTGCGAGCTGTGTCGAATCAACGCCGACCGCGTACCCGTCAC	120
Qy	121	TTCAAGTCTAAGGAGCTTCCCACTCCGCCCTGTCGAATCAACGCCGACCGCGTAC	180
Db	121	TTCAAGTCTAAGGAGCTTCCCACTTCGCCCTGTCGAATCAACGCCGACCGCGTAC	180
Qy	181	GTCAACCGCGCCCGTGGTGGCGCAATTCGGTGTGTCGAATCAACGCCGACCGCG	240
Db	181	GTCAACCGCGCCCGTGGTGGCGCAATTCGGTGTGTCGAATCAACGCCGACCGCG	240
Qy	241	CGTGAAGTGGCAGCGAAATTCGAATAGCAACCAAGCAGAGAAAGCTGCTGTTTCAA	300
Db	241	CGTGAAGTGGCAGCGCAATTCGGATAGCAACCAAGCAGAGAAAGCTGCTGTTTAA	300
Qy	301	GAAGTGATGTTCTGTTTATACGGTTCAAAGGAAATAAATCTTCAACAACTTAAAGC	360
Db	301	GAAGTGATGTTCTGTTTATACGGTTCCAAAAGGATATAAATCTTCAAGCTTAAGAT	360
Qy	361	GAAATTCATAACGTAATCCGATCGAATTTAGGACATCAGAAAGGAAATATAAAA	420
Db	361	AAAATTCATACGCAATCTTAATGTAGAAATTTAGGACATCAGAAATATAAAA	420
Qy	421	TATGATTTAAATTTGTAGATCAGGTTATGTATA---TGTAAGGAAAGATGAAAT	477
Db	421	TATGATTTAAATTTGTAGATCAGGTTATGTATACTACAAAGGAAAGATGAAAT	480
Qy	478	AAGTGACATTCAGATTACAAAGAGTTTCCAAACCGCTTAGGTTATGACGGTTTGTATAT	537
Db	481	GAGTGACATTCAAATCACAAAGCAGTTTACCTACCGGTTTGGTTATGACGGTTTGTATAT	540
Qy	538	TATTCGGAGAGAGCTCTTCCCAATCTTTACCGAGTGGCGGACCGTGAATATCTCGT	597
Db	541	TATTCGGAGAGACATCTTTTCGAATCTTTACCGAGCGCGGAAACCGTGAATATCTCGGC	600
Qy	598	AACTGGCAATATATGACCGATCCAAACGTCATCGAGCAGGTAAGGC---GGTTGCAAT	654
Db	601	AACTGGCAATATATGACCGATGCCATCGTATCTGAAACAGGAAAGCAGGAGATCTTAGC	660

Qy	655	GACAAATTTGGTTATTACACATTTTATGGTAAACGATGTGGTGCAACTTCTTATGCGGCT	714
Db	661	GAAGATTTGGTTATTATCGTTTATTCGGTCAAAATTCGGAGCACTTCTTATGCTGG	720
Qy	715	AAGGATGTCGACGAAAGGAGAAAACATCCTGCTAAATATACGGTAGATTTCCGTTACAAA	774
Db	721	ACTGCCGACGACCGAGAGGAGAAAACATCCTGCCGAATATACGGTAGATTTCCGTTAAGAAA	780
Qy	775	ACCTGAGGGCGAGCTGATTTAAACCAATATGT---CAAAACCGAGTGAGAACAAA	831
Db	781	ACTTTGACGGTAAATTAATTTAAATAATCAGTATGTGCAAAAGAAAACCGATGAAAGAAA	840
Qy	832	CCGCTGACCAATTAACATCATCTGCGATTAAACGGCAACCGCTTTTACCGGAGTGCC	891
Db	841	CCGCTGACCAATTTACGACATTTACTGCAACATTTGACGGCAACCGCTTTTACCGGAGTGCC	900
Qy	892	AAGGTCAATCTGATTTTAGCGAAAAGCAATGCAATTAAGGAGCAATTTGTTTTTCATGCC	951
Db	901	AAAGTTAAACCGAGGTGAAGACGAAACACGCTGATAAAGAGCATTTGTTTTTCATACC	960
Qy	952	GATCGGATCAGCGCTTTGAGGGCGGTTTTTTCGCGATTAAGGGGAGAGCTTTGCCGA	1011
Db	961	GATCGGATCAGCGCTTTGAGGGCGGTTTTTTCGCGATTAAGGGGAGAGCTTTGCCGA	1020
Qy	1012	CGGTTTATCAGCAACGACACAGCGTATTCGGTGTATTTCGAGGCAACAAAATAGCCCC	1071
Db	1021	CGGTTTATCAGCAACGACACAGCGTATTCGGGTTATTCGAGGCAACAAAATAGCAC	1080
Qy	1072	G-----TGCGCTCTGGAACACACACAAAATCTTG	1101
Db	1081	GCATCAACCGCATCAGATACAAATCCTGCTATGCGTCTGAAACACACACAAAATCTTG	1140
Qy	1102	GATTTCTGAAAAATTTTCGTTGATGAGCAAGTGGTGAATTTCCCGACCGTTTGCCAT	1161
Db	1141	GATTTCTGAAAAATTTTCGTTGATGAGCAAGTGGTGAATTTCCCGATTTGCCAT	1200
Qy	1162	TCTCCTATGCGCGATTTTGGTTCATCCCGACAACTCTTTCGAGAGGCGATGAAATCTCT	1221
Db	1201	TCCCTATGCGCGATTTTGGTTCATCCCGACAACTCTTTCGAGAGGCGTGAATCTCTC	1260
Qy	1222	TTGTTAGCCAAAGAAAAACCATCGAGCTTCCGACGGCAGGAAAATGACCGTCACTGCT	1281
Db	1261	TTGTTCAAGATACATCAAAACCATCGATCTTCCGACGGCAGGAAAATGACCGTCACTGCT	1320
Qy	1282	TGTTGCGACTTTTGAACCTATGTGAAACTCGGACGGATAAAAACCGAACCGCCCCCGCC	1341
Db	1321	TGTTGCGACTTTTGAACCTATGTGAAACTCGGACGGATAAAAACCGAACCGCCCCCGCAAGT	1380
Qy	1342	AAACCGAGGCGCAGGACGAAAGA---GGATTTCGACATTTGATAATGGCGAAGAAAGCGAA	1398
Db	1381	AAACCAAGGCGGAGAGATGAAATTTCCGAAGATGAAATTTGGTGAAGCGAGGAAATGAA	1440
Qy	1399	GACGAAATTCGGCGATGAAGAGAGAGCGACCGAAGATGACCGCGCAGGAGATGAAGCAGC	1458
Db	1441	GAGGATTTGGTTCGCTGAAGAGAGAAACACGGAAGACGAAAGTCTGTAAGATGAAGACAGA	1500
Qy	1459	GAAGAAGCGAAGCCACAGAAAAC-----	1482
Db	1501	GAAGAAGCGAAGTTTCCGAAGATGGTAAACAGTGAAGACGAGAAAGAAATCCCGAAGAA	1560
Qy	1483	-----GAAGACGGCGAGAGACGAAAGCTGAAGAACCTGAAGAAATTCGTCGACAGAA	1536
Db	1561	GATGATGATGAAGCGAAGAGAGGAAAGTTGAAGAACCGGAAGAAATTCGCGGAGAA	1620
Qy	1537	GGCAAC---GGCAGTTCAAAACCGCATCTGCTGCTCCCGGAGCGCTCTAAAGCGCAGGAT	1593
Db	1621	GGCGGGTGGCGGTTTCAGACGGCATCCCGCCGCTTCGGAAGCCCTTAAAGCGAGGAC	1680
Qy	1594	ATFCGACCTTTCTCTGAAAGGTTATCGCAGCGGAGAAAACGAATATTTCCGCAAACTCGAGAA	1653
Db	1681	ATCGACCTTTCTCTGAAAGGTTATCGCAGCGGCGGAGGCGACATTTCCGCAAACTCGAAAA	1740

QY 778 CTGACGGCGAGCTGATTAAACCAATATGTCACAAACCCAGTGAAGC---AAAAACCG 834
DB 781 CTGGAAGGTAGTGTATTAATAATCAGTATGTCAAAAGAGAGATGATCTTAATAATCCA 840
QY 835 CTGACCAATTTACAAATACATCAGTTCGATTTAAACGCGCAACCGCTTTACCGGCGAGTGCCAAAG 894
DB 841 CTGACCAATTTACAAATACATCAGTTCGATTTAAACGCGCAACCGCTTTACCGGCGAGTGCCAAAG 900
QY 895 GTCAATCTGATTTAGCGAAAGCGATGCGCAATAGAGAGATTTGTTTTCATGCGCGAT 954
DB 901 GTTAGCACCGAGGTGAAGACGACACACGCTGATTAAGAATATTTGTTTTCATACCGGAT 960
QY 955 GCCCATCAGCGGCTTGAGGGCGGTTTTTTCGCGCATAGGGGAGAGCTTTGCCGCGAG 1014
DB 961 GCCCATCAGCGGCTTGAGGGCGGTTTTTTCGCGCATAGGGGAGAGCTTTGCCGCGAG 1020
QY 1015 TTTATCAGCAACGACCAACAGCGTATTCGGTGATTTTCGCGAGCAACCA 1061
DB 1021 TTTATCAGCAACGACCAACAGCGTATTCGGTGATTTTCGCGAGCAACCA 1080
QY 1062 -----AAATAGCCCGTGCCTGCTGGAACACACCAAAATCTTGAT 1104
DB 1081 GCAAAACGATCAGATACAAATCTGCTGCTGCTGGAACACACCAAAATCTTGAT 1140
QY 1105 TCTCTGAAATTTCCGTTGATGAGCAAGTGTGAAATCCCGACCGTTTGCCATTTCT 1164
DB 1141 TCTCTGAAATTTCCGTTGATGAGCAAGTGTGAAATCCCGACCGTTTGCCATTTCT 1200
QY 1165 CCTATGCCCGATTTTGTTCATCCGACAAATCTTCTGCGAAGGCGATGAAATCTCTTTG 1224
DB 1201 ACTATGCCCGATTTTGTTCATCCGACAAATCTTCTGCGAAGGCGATGAAATCTCTTTG 1260
QY 1225 GTTAGCAGGAAACCATCAGCTTCGCGACGCGAGCAAAATGACCGTCACTGCTTGT 1284
DB 1261 GTTAGCAGGAAACCATCAGCTTCGCGACGCGAGCAAAATGACCGTCACTGCTTGT 1320
QY 1285 TGCGACTTTTGTGACCTGTGAAATCTGCGACGATGAAACCGACGCGCGCCGCCAAA 1344
DB 1321 TGCGACTTTTGTGACCTGTGAAATCTGCGACGATGAAACCGACGCGCGCCGCCAAA 1380
QY 1345 CCGAAGGCGCGAGGACGAGAGGATTCGACATTTGATAATGCGGAGAAAGCGAAGCA 1404
DB 1381 CCGAAGGCGCGAGGACGAGAGGATTCGACATTTGATAATGCGGAGAAAGCGAAGCA 1440
QY 1405 ATCGGCGATGAAGAGAGGACCGAAGATGCGCGAGGAGTGAAGGCGAGCGAAGAA 1464
DB 1441 ATTTCCGAAGATGATAACGCGGAGATGAAGTCAACCGAAGAGAGGAGCTGAAGAAAC 1500
QY 1465 GACGAAGCCACAGAAAACGAGACGCGAAGAA----- 1497
DB 1501 GAAGAGAACTGATGAAGACGAGAGAGAGAACCCGAGAAACTGAAGAACTGAAGAA 1560
QY 1498 -----GACGAAGCTGAAGAACCTGAAGAGAAATCTGCG---GCAAGAGGCAAC 1542
DB 1561 ACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCTGCGACGAGAGAGGCAAC 1620
QY 1543 GCGAGTTCAACGCGATCTGCTGCTGCGGAGGCTCTAAGGCGAGGATATCAACCTT 1602
DB 1621 GCGGTTTCAAGGAGATCTGCTGCTGCGGAGGCTCTAAGGCGAGGATATCAACCTT 1680
QY 1603 TTCTGGAAGGTATCGGACGCGAGAAACGATATTTTCGCAACTGGAGAGACGCTAT 1662
DB 1681 TTCTGGAAGGTATCGGACGCGAGGAGCGGACATTTCCCAATTTGGAAGAGCGCTAT 1740
QY 1663 ACCGCGACTTTGGAAGCGGATTCGCGCAACCCATTTCAATGGGACAAATCATCGGAT--- 1719
DB 1741 ACCGCGACTTTGGAAGCGGATTCGCGCGGCGGATTAAGAGGCGAAGAGCTAGATGCG 1800
QY 1720 -----AAAGAGCGGCAAGAGCTATTTTACCGTT 1749
DB 1801 ACTAGCTCCATTCAAAAGGATAGTATGCAATCAAGCGGCAAGAGCAATTTGACGTT 1860
QY 1750 GATTTCCGCAAGAAATCGATTTCCGGAACGCTGACGAGAAACCGTGTAGAACCTGCT 1809

DB 1861 GATTTTGTGCGAAGTGCCTTTAGGTAAGTTGACAGAAAAAATGATACACCCCGCT 1920
QY 1810 TTCCGTTATGAAAACGCGGTGATTCAGGCGAACGTTTCCATGCGACAGCGCGCTCGG 1869
DB 1921 TTTTATATGAAAAGGTGATTCAGGCGAACGTTTCCACGCTTTGGCGCGTACTCGT 1980
QY 1870 GATCAGCGCATCGACCTTTTCGCGGCGAGGTTTCGACCAACCGCAGATCTTCAAAGCTAAT 1929
DB 1981 GAAAATGTTGATTTGTTCTGCGCAAGTTTCGACTATCCCAAAGTTTAAAGCCAGT 2040
QY 1930 GATCTTCGTGAGAGAGGATTTTACGCCCGAAGCGGAGGAATTTGGCGGATTAAT 1989
DB 2041 AATCTTCTGTAAGAGGAGGATTTATGTTCCGCGAGCGGAGAGTTGGTGGTAAATAT 2100
QY 1990 TTCAATATGATGGAAA 2007
DB 2101 ATCAGCAGTGCACCGAAA 2118

RESULT 8
AA23323
ID AA23323 standard; cDNA; 2124 BP.
XX
AC AA23323;
XX
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain 881607 LbpB cDNA.
XX
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
CDS 1. 2124
FT /*tag= a
FT /product= "LbpB"
XX
FN WO9909176-A1.
XX
PD 25-FEB-1999.
XX
PR 10-AUG-1999; 98WO-EP005117.
XX
PR 15-AUG-1997; 97GB-00017423.
XX
PR 05-FEB-1998; 98GB-00002544.
XX
(UYUT-) RIJKSUNIV UTRECHT.
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX
PI Pettersson-Fernholm AM, Tommassen JPM;
XX
WPI; 1999-190165/16.
DR P-PSDB; AAW93496.
XX
PT New lactoferrin-binding protein B polynucleotides - obtained from
PT Neisseria meningitidis, used to develop products for the diagnosis,
PT prevention and treatment of neisserial disease, e.g. meningitis.
XX
PS Claim 2; Page 105-109; 116pp; English.
XX
CC This invention describes novel lactoferrin-binding protein B (LbpB)
CC strains of Neisseria meningitidis. The products of this invention can be
CC used for vaccinating humans against neisserial disease e.g. meningitis.
CC Antibodies raised against the proteins of the invention can be used for
CC diagnosing or treating neisserial disease in humans. The LbpB
CC polypeptides can also be used for identifying compounds which inhibit the
XX polypeptides
XX
Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;

[Handwritten signature]

QY 1720 AAAGACGGCGAAACAGCATATTTCACGTTGATTCGCGCAAGAAATCGATTCGCGAAGC 1779
Db |||||
13587 AAAGAACGGCGAAACAGCATATTTCACGTTGATTCGCGCAAGAAATCGATTCGCGAAGC 13528
QY 1780 CTGACGGAGAAACCGGTGAGAACCTGTTCCGTTATTCGAAACCGCGTGATTTGAGGGC 1839
Db |||||
13527 CTGACGGAGAAACCGGTGAGAACCTGTTCCATATTGAAACCGCAAGATTGAGGGC 13468
QY 1840 AACGGTTTCATCCGACAGCGCCACTCCGGATGACGGCATCGACCTTCCCGGGCAGGGT 1899
Db |||||
13467 AACGGTTTCATCCGACAGCACGCACTCCGGAGAACGGCATCAATTTCCGGGAATGGT 13408
QY 1900 TCGACCAACCGCAGATCTTCAAAGTAATGATCTTCGTGTAGAGAGGATTTACGGC 1959
Db |||||
13407 TCGACCGACCCCAAAACCTTCCAAGCTAGTAATCTTCGTGTAGAGGGGATTTACGGC 13348
QY 1960 CCGAGCGGAGAAATGGCGGTATATTTCAATAATGATCGGAANTCTCTGGTATA 2019
Db |||||
13347 CCGAGCGGAGAAATGGCGGTATATTTCAATAATGATCGGAANTCTCTGGTATA 13288
QY 2020 ACTGAAGGTACTGAAATAAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTT 2079
Db |||||
13287 ACTGAAGGTACTGAAATAAAGTTGATGTTGAAGCTGAAGTTGATGTTGATGTTGATGTT 13229
QY 2080 GATGCTGATGCTGATGTTGAACAGTTAAACCTGAAGTTAAACCCCAATTCGCGGTGTA 2139
Db |||||
13228 -----TGGCAACAGTTAGATCTGAAGTTAAACACCAATTCGCGGTGTA 13183
QY 2140 TTCGTCGCAAGAAAGATATAAGAGGTGGAATA 2175
Db |||||
13182 TTCGTCGCAAGAAAGATATGACGAGGAGTGGAAAA 13147

RESULT 10

AAF91389
ID AAF91389 standard; DNA; 1000 BP.
XX AAF91389;
AC AC
XX AC
DT 04-MAY-2001 (first entry)
XX 04-MAY-2001 (first entry)
DE N. meningitidis (serogroup B) lbpA gene upstream sequence, SEQ ID:15.
XX
XX Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;
KW genetically modified; protective antigen expression; LPS detoxification;
KW LPS; lipid A; homologous recombination vector; immunisation;
KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.
XX
XX Neisseria meningitidis.
XX
XX WO200109350-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-EP007424.
XX
XX 03-AUG-1999; 99GB-00018319.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Berthet FJ, Dalemans WLJ, Denoel P, Dequesne G, Feron C, Lobet Y;
PI Poolman J, Thyry G, Thonnard J, Voet P;
XX WPI; 2001-138654/14.
XX
XX New isolated polynucleotide useful for outer membrane vesicle preparation
PT from Gram-negative bacterial strain for vaccination of microbial
PT infections.
XX
XX Claim 46; Page 81; 128pp; English.
PS
XX The invention relates to a genetically-engineered outer membrane vesicle
CC (bleb) preparation from a Gram-negative bacterium for use as a vaccine.
CC

CC The blebs of the invention are improved with respect to their
CC immunogenicity and toxicity by the introduction of one or more genetic
CC changes to the chromosome of the bacterium from which the blebs are
CC derived. The changes made include the upregulation of protective antigen
CC expression, the downregulation of immunodominant non-protective antigen
CC expression, and genetic changes which result in detoxification of the
CC Lipid A moiety of lipopolysaccharide (LPS). The invention also
CC encompasses modified Gram-negative bacterial strains from which the bleb
CC events (for the generation of the modified bacterial strains),
CC bacterially-derived nucleic acid sequences used in such a vector, and an
CC immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole
CC cell vaccine suitable for paediatric use. The bleb preparation is useful
CC in the manufacture of a medicament for immunising a human host against a
CC disease caused by infection of one or more of the following: Neisseria
CC meningitidis, Neisseria gonorrhoeae, Haemophilus influenza, Moraxella
CC catarrhalis, Pseudomonas aeruginosa, Chlamydia trachomatis, and Chlamydia
CC pneumoniae. The invention may also be used to provide immunisation against
CC the influenza virus. Bacterially derived nucleotide sequences of the
CC invention are used in the performance of homologous recombination events
CC up to 1000 bp upstream of a bacterial chromosomal gene in order to either
CC increase or decrease expression of that gene. Immunoprotective and non-
CC toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more
CC immunogenic, less toxic and safer, and are particularly useful for
CC paediatric use. The present sequence represents a specifically claimed
CC Neisseria meningitidis nucleic acid sequence
XX

Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;

Query Match 31.2%; Score 678.6; DB 4; Length 1000;
Best Local Similarity 82.4%; Pred. No. 1.6e-156;
Matches 830; Conservative 0; Mismatches 164; Indels 13; Gaps 4;

QY 1174 GATTTTGGTTCATCCCGACAAACTTCTTGTGCAAGGCGCATGAAATTCCTTTGGTTAGCCAA 1233
Db 1 GATTTTGGTTCATCCCGACAAACTTCTTGTGCAAGGCGCGTGAATTCCTTTGGTTAGCCAA 60
QY 1234 GAGAAAACCATCGAGCTTCCCGACGCGAGAAATACCGTCACTGTTGTTCCGACTTT 1293
Db 61 GAGAAAACCATCAAGCTTCCCGATGCGAGGAAATGACCGTCCGTTCTTTCGACTTT 120
QY 1294 TTGACCTATGTGAACTCGGACGGATATAAACCGAACGCCGCCGCCAACCGAGGGCG 1353
Db 121 TTGACCTATGTGAACTCGGACGGATATAAACCGAACGCCGCCGCCAACCGAGGGCG 180
QY 1354 CAGGACGAA---GAGGATTCCGACATTTGATTAATGCGGAGAAAGCAAGCAAAATCGGC 1410
Db 181 GAGATAAAGGAGGAGATGAGAGAGTGCAGGCGTTGTTAACTCGAGAGCGGAGGC 240
QY 1411 GATGAAGAGAGAGGACCGAAGATGCGCGCAGGAGATGAAGCGAGCGAGAGAGCGAA 1470
Db 241 GAAATTTCCGAAATGAAGCGGAGAAAGCGCGAAGAAATCGTCGAGAGAACCCGAGAA 300
QY 1471 GCCACAGAAACGAGACGGCGAGAGAGCGAGCTGAGACCTGAGAGAGATCGTCG 1530
Db 301 GAAGCTGAAGAGAGAGAGAGCTGAACCCCAAGAGTTGAAGAAACCCGAGAGAAATCGCCG 360
QY 1531 GCAGAGAGGCAACGGCA---GTTCAAAACGGCATCTCTGCTGTCCCGAAGCCTCTAAAGGC 1587
Db 361 ACAGAGAGAGAGCGGACGCGTTCAACGCGCATCTCTGCTGTCCGAGCCTCTAAAGGC 420
QY 1588 AGGGATATCGACCTTTTCTGAAAGGTATCCGACGCGGAGAAACGAAATATTCGCGAACT 1647
Db 421 AGGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAGAGCCGACATTCGAGAAC 480
QY 1648 GGAAGAGACGCTATACCGGCATCTCGGAGCGCGCTATCGGCAACCCATTCATGGGAC 1707
Db 481 GGAAGAGACGCTATACCGGCATCTCGGAGCGCGCTATCGGCAACCCATTCATGGGAC 540
QY 1708 AATCATCGCGGATAAAGAGCGGCAAAAGCAGTATTTACCGTTGATTTCCGCAAGAAATCG 1767
Db 541 AATCATCGCGGATAAAGAGCGGCAAAAGCAGTATTTACCGTTGATTTCCGCGGAGAAATCG 600


```
QY 1768 ATTTCCGGAACGCTGACGGAGAAAAACGGGTAGAACCTGCTTTCGGTATTGAAAAAGCGC 1827
Dd |||||
QY 601 ATTTCCGGACCTGACGGAGAAAAACGGGTGACACCTGCTTTCTATTATTGAAAAAGCGC 660
Dd |||||
QY 1828 GTGATTGAGGGCAACGGTTTCCATCGCAGCGCGCACTCGGGATGACGGCATCGACCTT 1887
Dd |||||
QY 661 AAGATTGAGGGCAACGGTTTCCACGCAACAGCACGCACTCGTGAGAACGGCATCAATCTT 720
QY 1888 TCGGGCAGGGTTCACCAACCGCAGATCTTCAAGCTAATGATCTTCGTAGAGGA 1947
Dd |||||
QY 721 TCGGAAATGGTTTCACCAACCGCAGACCTTCCAAGCTAGTGTCTTGGTGAAGGA 780
QY 1948 GGATTTTACGGCCCGAAGCGGAGGAATGGCGCGTATTATTTCATTAATCATCGGAAA 2007
Dd |||||
QY 781 GGATTTTACGGCCCGCA-GCGAGAGATTTGGCGGTATTATTTCATTAAGATGGGAAA 839
QY 2008 TCTCTTGTATTAACCTGAAGTACTGAAATAAAGTTGAAGCTGATGTTGATGTTGATGTT 2067
Dd |||||
QY 840 TCTCTTGTATTAACCTGAAGTACTGAAATAAAGTTGAAGTGAAGCTGAAGTTGAAGTT 899
QY 2068 GATGTTGATGTTGATGCTGATGCTGATGTTGAACAGTTAAACCTGAAGTTAAACCCCA 2127
Dd |||||
QY 900 GAAGCTGAACCTGGTGTGTCGAACAGTTAGAAC-----CTGATGAAGTTAAACCCCAA 953
QY 2128 TTCCGCGTGGTATTTCGGTCCGAAGAAAGATAATAAAGAGGTGAAAA 2174
Dd |||||
QY 954 TTCGCGTGGTATTTCGGTCCGAAGAAAGATAATAAAGAGGTGAAAA 1000

RESULT 11
ABK37769
ID ABK37769 standard; DNA; 1000 BP.
XX
AC ABK37769;
XX
DT 08-MAY-2002 (first entry)
XX
DE DNA sequence upstream of LbpA #1 gene.
XX
KW Upstream sequence; ds; Antibacterial; vaccine; bleb;
KW Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;
KW meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;
KW sinusitis.
XX
OS Neisseria meningitidis serogroup B.
XX
FN WO200209746-A2.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-EP008857.
XX
XX 31-JUL-2000; 2000WO-EP007424.
PR 08-FEB-2001; 2001GB-00003170.
XX
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Berthet FJ, Dalemans W, Denoel P, Dequesne G, Feron C, Garcon N;
PI Lobet Y, Poolman J, Thirry G, Thonnard J, Voet P;
XX
XX WPI; 2002-188688/24.
XX
XX New immunogenic composition comprising an antigen derived from a pathogen
PT and a blep preparation from Neisseria meningitidis, useful as a vaccine
PT for treating or preventing disease caused by the pathogen.
XX
XX Disclosure; Page 84; 125pp; English.
XX
XX The invention relates to an immunogenic composition comprising an antigen
CC derived from a pathogen capable of protecting a host against the
CC pathogen, mixed with an adjuvant comprising a blep preparation derived
CC from a Gram-negative bacterial strain. The immunogenic composition
CC consists of N. meningitidis B blebs or N. meningitidis C polysaccharide
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CC antigen. The blebs (derived from the outer membrane) may also have their
CC toxic lipopolysaccharide (LPS) content reduced using heterologous down
CC regulating sequences for LPS pathway genes or by up regulating genes
CC involved in LPS synthesis suppression, by a promoter replacement
CC technique. The immunogenic preparation is useful in the manufacture of a
CC medicament for the treatment of a disease caused by the pathogen from
CC which the antigen is derived (e.g. from Neisseria, meningitis and
CC bacteraemia, from Moraxella, otitis media and pneumonia, and from H.
CC influenzae chronic bronchitis, sinusitis, pneumonia and otitis media).
CC The bleb derived from M. catarrhalis or from a non-typeable H. influenzae
CC is useful as an adjuvant in an immunogenic composition comprising one or
CC more pneumococcal capsular polysaccharides or protein antigens. The
CC present sequence is an upstream sequence from an N. meningitidis.
CC H. influenzae or M. catarrhalis gene involved in LPS biosynthesis, which
CC either up regulates or down regulates sequences to which it is attached
XX
SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;
Query Match 31.2%; Score 678.6; DB 6; Length 1000;
Best Local Similarity 82.4%; Pred. No. 1.6e-156;
Matches 830; Conservative 0; Mismatches 164; Indels 13; Gaps 4;
QY 1174 GATTTTGTGTCATCCCGACAAACTTCTGTGGAAGGGCATGAAATTCCTTTGTTAGCCAA 1233
Dd |||||
QY 1234 GAGAAAACCATCGAGCTTGGCGACGCGAGGAAATGACCGTCAGTCTGTTGCGACTTT 1293
Dd |||||
QY 61 GAGAAAACCATCAAGCTTGGCGATGGCAGGGAATGACCGTCCGTGCTTGTTCGACTTT 120
QY 1294 TTGACCTATGTGAACTCGGACGATGAAACCGAACCCCGCGCAAGTAAACCAAGGGC 180
Dd |||||
QY 1354 CAGGACGAA--GAGGATTCGACATTTGATATGCGAAGAAAGCGAAGACGAAATCGCG 1410
Dd |||||
QY 181 GAAGATAAAGGGAGGATGAAGAGAGTGCAGGCGTTGTTGTAAGTCGAGAGAGCGGAGGC 240
QY 1411 GATGAAGAAGAGGACCGCAGAGATCGACGCGCAGAGATGAAGCGGACGAGCAAGAACGAA 1470
Dd |||||
QY 241 GAAGTTCGGAAGATGAAGGCGAAGAACCGCAAGAAATCGTGAAGAAAGAACCCGAAAGAA 300
QY 1471 GCCACAGAAAACGAGACGGCGAAGACGAAAGCTGAAGACCTGAAGAAAGTGAAGAAATCGTCG 1530
Dd |||||
QY 301 GAAGCTGAAGAGGAAGAGAGCTGACCCAAAGAGTTGAAGAAACCGAAGAAATTCGCGCG 360
QY 1531 GCAGAGGCAACGGCA---GTTCAAACGCCATCTCTGCTGTCTCCGGAAGCCCTCTAAAGCG 1587
Dd |||||
QY 361 ACAGAAAGAAAGCGCAGCGGTTCAAACGCCATCTCTGCTGCTCGGAAGCCCTCTAAAGCG 420
QY 1588 AGGGATATCGACCTTTTCTGAAAGGTATCGCAGCGGAGAAACGAAATATTCGCAAACT 1647
Dd |||||
QY 421 AGGGACATCGACCTTTTCTGAAAGGTATCGCAGCGGGAAGCGGACATTCCTCAAGAAC 480
QY 1648 GGAGAAGCAGCGCTATACCGGCACCTTGGGAAGCGCTGTCGGCAACCCCATTCATGGGAC 1707
Dd |||||
QY 481 GGAAAGCACATATACCGGCACCTTGGGAAGCGGCTATCGGCACACCCCATTCATGGGAC 540
QY 1708 AATCATGCGGATTAAGAGAGCGGCAAAAGCAGTATTACCGTTGATTTCGGAAGAAATTCG 1767
Dd |||||
QY 541 AATCAGGCGGATTAAGAGAGCGGCAAAAGCAGTATTACCGTTAATTTTCGGCGAGAAATCG 600
QY 1768 ATTTCGGAAACGCTGACGGAGAAAAACGGGTGAGAACCTGCTTTCGTTGATTGAAACCGCG 1827
Dd |||||
QY 601 ATTTCCGGAACGCTGACGGAGAAAAACGGGTGACAAACCTGCTTCTATATTGAAAAAGCGC 660
QY 1828 GTGATTGAGGGCAACGGTTTCCATGCGACAGCGCACTCGGATGAGGGATCGACCTT 1887
Dd |||||
QY 661 AAGATTGAGGGCAACGGTTTCCACGCAACAGCACGCACTCGTGAGAGAGCGGATCAATCTT 720
QY 1888 TCCGGGCGAGGGTTCGACCAAAACCGCAGATCTTCAAAGCTAATGATCTTCGTGTAAGGA 1947
Dd |||||
QY 721 TCGGAATATGGTTGACCCAAACCCAGAACCTTCCAAAGCTAGTATCTTCGTGTAAGGA 780
```

QY 1948 GGATTTTACGGCCCGGAGGAGGATTTGGCGGTATTATTTTCAATATGATGGAAA 2007
 Db |||||
 781 GGATTTTACGGCCCGCA-GCGAGGATTTGGCGGTATTATTTTCAATAGGATGGAAA 839
 QY 2008 TCTCTTGGTATAACTGAAGTACTGAAATTAAGTTGAAGCTGATGTTGATGTT 2067
 Db |||||
 840 TCTCTTGGTATAACTGAAGTACTGAAATTAAGTTGAAGTTGAAGTTGAAGTT 899
 QY 2068 GATGTTGATGTTGATGCTGATGCTGATGTTGACAGTTAAACCTGAAGTTAAACCCAA 2127
 Db |||||
 900 GAAGCTGAACACTGGTGTGTCGAACAGTTAGAAC-----CTGATGAAGTTAAACCCAA 953
 QY 2128 TTCCGGCGTGTATTTCGGTGCAGAAAGATAATAAAGAGGTGAAAAA 2174
 Db |||||
 954 TTCCGGCGTGTATTTCGGTGCAGAAAGATAATAAAGAGGTGAAAAA 1000

RESULT 12
 AAA81815
 ID AAA81815 standard; DNA; 707 BP.
 XX
 AC AAA81815;
 XX
 DT 04-DRC-2000 (first entry)
 XX
 DE N. meningitidis partial DNA sequence gpm_362 SEQ ID NO:362.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MenB; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN WC200022430-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US023573.
 XX
 PR 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V;
 PI Rappuoli R, Pizza M;
 XX
 DR WPI; 2000-318079/27.
 XX
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 XX
 PS Claim 7; Page 1606; 1760pp; English.
 XX
 CC The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding PCR primers; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament for in the manufacture of a medicament for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium

CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions

XX Sequence 707 BP; 199 A; 155 C; 178 G; 173 T; 0 U; 2 Other;

QY Query Match 21.2%; Score 460.4; DB 3; Length 707;
 Db Best Local Similarity 79.3%; Pred. No. 6.4e-103;
 Matches 561; Conservative 0; Mismatches 137; Indels 9; Gaps 1;

QY 23 GCATTTGCTGTTGGCCCTTACCTTTTGGCATCTTTGTATCGCGCAATTTGGCGTGCAGC 82
 Db 1 GCATTTGCTGTTGGCCCTTACCTTTTGTATCGCGCAATTTTCGGCGTGCAGC 60
 QY 83 CTGTTGTGCAATCAACGCGCAGCGCTACCCCGTCACTTTCAAGTCTTAAGGACGTTCCCA 142
 Db 61 CTGTTGTGCAATCAACGCGCAGCGCTACCCCGTCACTTTCAATCTAAGGACGTTCCCA 120
 QY 143 CTCGCCCTCTGCCAAACCTTTTATAGAAATACGCGGTCAACCGCCCGCGTGGTG 202
 Db 121 CTCGCCCTCTGCGGGTCTTCGGTAGAAACCAACGCGGTCAACCGCCCGCGTGGTG 180
 QY 203 CGCAATGCGGTGCCAAGCGCAATCTGCTTTTCATCGTGAAGTGGCACGGAATTC 262
 Db 181 CGCAATGCGGTGCCAAGCGCAATATTGCTTCTTATAAACAAGACGCTACCGAATTC 240
 QY 263 CAAATAGCAAAACAAGCAGAGAAAGCTGTCGTTTCAAGAAAGGTGATGTTCTGTTTTAT 322
 Db 241 CCGACAGCATCAGGACAGGAGCATCTGCGCTTAAAGAGAGGATATCTCTGTTTTAG 300
 QY 323 ACGGTTCAAAAGGAAATAAACTTCAACAACTTAAAAAGCGAAATTCATAAAGTGATTCG 382
 Db 301 ACGGTACGCTGAAAGAACAGGCTGACAACTTAAAAAGAAATCAACGAACGGTATTCTG 360
 QY 383 ATGTAGAAATTAGGACATCAGAAAGGAAATTAAGTAATGATTAATTAATTTCTAGATG 442
 Db 361 ATGTAGGGGTTATCATATCGAAAAAAGAGAAAGAAATATCAATATCAATTTGTCGGTG 420
 QY 443 CAGGTTATGATATGTAAGGGGAAAG-----ATGAAATTAAGTGGACTTCAGATT 493
 Db 421 CGGCTATGTTTACCAGCGCGGAGGAGGATATGAAAGAAAGACATCTGATG 480
 QY 494 ACAAGCAGTTTCCAAACCGCTTAGGTTATGACCGGTTTTGATATATTCGGAAGAGTC 553
 Db 481 GTAAGGAGTTTGTAAACCGATTTAGTTATGACGGTTTTGATATATTCGGAAGAGTC 540
 QY 554 CTTCCCAATCTTTACCGAGTCGCGGAACGGTGAATATTTCTGTAATCGCAATATGA 613
 Db 541 CTTCCCAATCTTTACCGAGCGCGGAACGGTGAATATTCGGAATCGCAATATGA 600
 QY 614 CCGATGCCAAACGCTCATCGAGCAGGTAAGCGGTGCGCATTTGCAATTTGGGTTATTACA 673
 Db 601 CCGATGCCAAACGCTCATCGACANGTAAGCGGTTTCAGTACGATTGGGTTATACCA 660
 QY 674 CATTATGATGAACGATTTGGTGCAACTTCTTTATCGCGCTAAGGAT 720
 Db 661 CATATTATGTAATGAAATTTGGGCAACTTCTTTATGAGGCTAGGAT 707

RESULT 13

ABS67377

ID ABS67377 standard; DNA; 3300 BP.

XX ABS67377;

DT 29-NOV-2002 (first entry)

XX

DE Neisseria gonorrhoeae lbpA gene.
 XX Gram-negative bacterial bleb; PorB; outer membrane protein;
 KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
 KW protective antigen; antibacterial; vaccine; gene; ds.
 XX Neisseria gonorrhoeae.
 OS
 XX WO200262380-A2.
 FN
 XX 15-AUG-2002.
 PD
 XX 08-FEB-2002; 2002WO-EP001356.
 PP
 XX 08-FEB-2001; 2001GB-00003169.
 PR
 XX (SMIK) SMITHLINE BEECHAM BIOLOGICALS.
 PA
 XX Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
 PI
 XX WPI; 2002-657510/70.
 DR
 XX P-PSDB; ABG31056.
 DR
 XX Novel gram-negative bacterial bleb presenting on its surface PorB outer
 PT membrane protein from Chlamydia trachomatis or protective antigen from
 PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.
 PT
 XX Disclosure; Page 48-49; 75pp; English.
 PS
 XX The present invention relates to a new gram-negative bacterial bleb
 CC presenting on its surface the PorB outer membrane protein from Chlamydia
 CC trachomatis, or a protective antigen from C. pneumoniae. The invention is
 CC useful for preventing C. trachomatis or C. pneumoniae infection in a
 CC host. The present nucleic acid sequence represents a Neisseria
 CC gonorrhoeae gene as described in the invention
 CC
 XX Sequence 3300 BP; 897 A; 807 C; 921 G; 675 T; 0 U; 0 Other;
 SQ
 Query Match 8.0%; Score 174.2; DB 6; Length 3300;
 Best Local Similarity 77.2%; Pred. No. 3.2e-32;
 Matches 240; Conservative 0; Mismatches 38; Indels 33; Gaps 1;
 QY 1865 CTCGGGATGAGCGGATCGACCTTCCGGGCGAGGTTTCACCAACCGCGATCTTCAAG 1924
 Db 1 CTCGGGATGAGCGGATCGACCTTCCGGGCGAGGTTTCACCAACCGCGATCTTCAAG 60
 QY 1925 CTAATGATCTTCGTGTAGAAGGAGGATTTACGGCCCGAAGCGGAGGAATTTGGCGGTA 1984
 Db 61 CCGACAACTTCTTGTAACGGGCGGCTTTACGGCCCGCGAGGCGGAATTTGGCGGCA 120
 QY 1995 TTATTTCAATAAGTATGGGAAATCTCTTGATTAATCTGAGGTAAGTAAAGTTG 2044
 Db 121 CTATTTTCAATAAGTATGGGAAATCTCTTGATTAATCTGAGGTAAGTAAAGTTG 180
 QY 2045 AAGCTGATGTTGATCTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2104
 Db 181 AAATGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 207
 QY 2105 TAAACCTGAGATTAACCCCAATTTCCGGCGTGGTATTCGGTTCGGAAGAAGATAATAAG 2164
 Db 208 TAGAACCTGAGTAAACCCCAATTTCCGGCGTGGTATTCGGTTCGGAAGAAGATAATAAG 267
 QY 2165 AGGTGGAATAA 2175
 Db 268 AGGTGGAATAA 278
 RESULT 14
 AAZ31947
 ID AAZ31947 standard; DNA; 2139 BP.
 XX
 AC AAZ31947;
 XX

DT 26-JAN-2000 (first entry)
 XX M. catarrhalis strain 3 tpbB gene.
 DE
 XX TbpB gene; Tbp2; transferrin binding protein; diagnosis; otitis media;
 KW genetic immunisation; Moraxella infection; antigen; vaccine; detection;
 KW antitumour antibody production; therapy; ss.
 OS
 XX Moraxella catarrhalis.
 OS
 XX WO9952947-A2.
 FN
 XX 21-OCT-1999.
 PD
 XX 12-APR-1999; 99WO-CA000307.
 PP
 XX 14-APR-1998; 98US-00059584.
 PR
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 XX Myers LE, Schryvers AB, Harkness RE, Loosmore SM, Du R, Yang Y;
 PI Klein MH;
 PI
 XX WPI; 1999-620376/53.
 DR
 XX P-PSDB; AAY43379.
 DR
 XX Nucleic acid encoding transferrin binding protein 2 of Moraxella
 PT catarrhalis, useful for diagnostics, immunization and recombinant protein
 PT production.
 PT
 XX Claim 2; Fig 4; 114pp; English.
 PS
 XX This sequence encodes the Moraxella catarrhalis strain 3 transferrin
 CC binding protein (Tbp2) of the invention. This sequence is also referred
 CC to as the TbpB gene. The tpbB gene is used to produce recombinant Tbp2;
 CC for identification or diagnosis of Moraxella, or for cloning related
 CC species, using hybridisation assays; and for genetic immunisation against
 CC Moraxella infections, e.g. otitis media. The Tbp2 proteins are useful as
 CC antigens, either in vaccines (including components of conjugate vaccines
 CC that contain antigens from other bacteria or from tumours, in which case
 CC they elicit production of antitumour antibodies that may be coupled to
 CC chemotherapeutic agents or biologically active agents) or to raise
 CC antibodies (for use as diagnostic reagents and for treating Moraxella
 CC infections), also for detecting Moraxella antibodies
 CC
 XX Sequence 2139 BP; 738 A; 406 C; 461 G; 534 T; 0 U; 0 Other;
 SQ
 Query Match 4.1%; Score 88.2; DB 2; Length 2139;
 Best Local Similarity 57.3%; Pred. No. 3.8e-11;
 Matches 184; Conservative 0; Mismatches 128; Indels 9; Gaps 1;
 QY 747 TAATATACGCTAGATTTTCGGTAAACAAACCTGACGGCGGCGTATTAAACCAATA 806
 Db 978 TGAGTTTACGCTAGATTTTCGGTAAACAAACCTGACGGCGGCGTATTAAACCAATA 1037
 QY 807 TGTCACAAACCGAGTGAAGCAAAACCGCTGACCAATTTACCAACATCACTGCCGATTAAA 866
 Db 1038 AGACCAACCATAGGCAAGGTTACGAAACCAACGCTATGACATCAATGCCGATATCCA 1097
 QY 867 CGGCAACCGCTTACCGGCGAGTCCCAAGGTCAATCTGATTAGCGAAAGCAATGCCAA 926
 Db 1098 CGGTAACCGCTTCGGTGGCAGTGCCACCGCAATCAATAAGATAATGAAGCAAGCAAA 1157
 QY 927 TAAGGAGCATTTGTTTTTCATGCCATGCCATGCGGCTTAGGGCGGTTTTTTTCGG 986
 Db 1158 ACA-----CCCTTTTACCAGCGATGCCCAATAGGCTAGAGGCGTTTTTATGG 1208
 QY 987 CGATAAGGGGAAGAGCTTGGCGGACGCTTTATACGAAACGACACACAGCTATTTCGGTGT 1046
 Db 1209 ACCAAACCGCGAGGAGCTGGCAGGTAAATTCCTAACCATGACACAACTCTTTGGTGT 1268
 QY 1047 ATTTCGAGGCAAAACAAATAG 1067

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	75.4	3.5	2127	4	US-08-778-570B-8
5	75.4	3.5	2127	4	US-09-059-584-8
6	75.4	3.5	3435	4	US-08-778-570B-7
7	75.4	3.5	3435	4	US-09-059-584-7
8	71	3.3	2230	3	US-08-448-194-7
9	71	3.3	2230	4	US-08-867-921-7
10	70.8	3.3	2145	4	US-09-059-584-48
11	70.8	3.3	2287	4	US-09-059-584-47
12	70.8	3.3	58909	4	US-09-596-002-30
13	69.2	3.2	929	4	US-09-671-317-14
14	69.2	3.2	1001	4	US-09-671-317-439
15	67.6	3.1	390	3	US-09-197-649-7
16	67.6	3.1	1276	3	US-09-177-325-2
17	67.6	3.1	1276	3	US-09-411-812A-2
18	67.6	3.1	1276	4	US-09-590-113-2
19	66.4	3.1	2256	6	5220013-1
20	65	3.0	2223	1	US-08-257-073-4
21	65	3.0	43795	3	US-08-742-185-101
22	64.8	3.0	2253	4	US-09-548-372D-56
23	64.8	3.0	2253	4	US-09-548-367D-56
24	64.8	3.0	2253	4	US-09-551-853D-56
25	64.8	3.0	2256	2	US-08-422-333-1
26	64.8	3.0	2256	6	5187153-1
27	64.8	3.0	2256	6	5223482-1

28 64.8 3.0 2259 4 US-09-548-372D-60 Sequence 60, Appl
29 64.8 3.0 2259 4 US-09-548-367D-60 Sequence 60, Appl
30 64.8 3.0 2259 4 US-09-551-853D-60 Sequence 60, Appl
31 64.8 3.0 2265 2 US-08-104-165-5 Sequence 5, Appl
32 64.8 3.0 2265 3 US-08-464-250-5 Sequence 5, Appl
33 64.8 3.0 2265 4 US-08-464-250-5 Sequence 5, Appl
34 64.8 3.0 2310 4 US-09-548-372D-54 Sequence 54, Appl
35 64.8 3.0 2310 4 US-09-548-367D-54 Sequence 54, Appl
36 64.8 3.0 2310 4 US-09-551-853D-54 Sequence 54, Appl
37 64.8 3.0 2310 4 US-08-685-649-2 Sequence 2, Appl
38 64.8 3.0 2313 1 US-08-133-248-7 Sequence 7, Appl
39 64.8 3.0 2316 4 US-09-548-372D-58 Sequence 58, Appl
40 64.8 3.0 2316 4 US-09-548-367D-58 Sequence 58, Appl
41 64.8 3.0 2316 4 US-09-551-853D-58 Sequence 58, Appl
42 64.8 3.0 3148 1 US-08-133-702-3 Sequence 3, Appl
43 64.8 3.0 3148 4 US-08-832-867-4 Sequence 4, Appl
44 64.8 3.0 3520 2 US-08-422-333-20 Sequence 20, Appl
45 64.8 3.0 8591 1 US-08-462-859A-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-059-584-50
; Sequence 50, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2139 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-059-584-50
Query Match 4.1%; Score 88.2; DB 4; Length 2139;

Best Local Similarity 57.3%; Pred. No. 5e-13;
Matches 184; Conservative 0; Mismatches 128; Indels 9; Gaps 1;
QY 747 TAAATACGGTAGATTTCGGTAACAAACCCCTGACGGGAGCTGATTAACAAACCAATA 806
Db 978 TGAATTACGGTAGATTTCGGTAACAAACCCCTGACGGGAGCTGATTAACAAACCAATA 1037
QY 807 TGTCAACACCGTAGGAGCAAAACCGCTGACCATTTTAAACATCACTGCCGATTTAA 866
Db 1038 AGACCAACCAAGGCAAGGTACGAAACCAACCGCTATGACATCAATGCCGATATCA 1097
QY 867 CGGCAACCGCTTACCGGAGTCCCAAGGTCAATCTGATTAGCAAAAGCCATGCCAA 926
Db 1098 CGGTAACCGCTTCCGTCGAGTCCCAAGGTCAATCTGATTAGCAAAAGCCATGCCAA 1157
QY 927 TAAGGAGCATTTGTTTTCATGCCGATGCCGCTTACCGGCTTACCGGCTTATTCGG 986
Db 1158 ACA-----CCCCCTTACCGAGTCCGCAATAGGCTAGAGGCGGTTTTATGG 1208
QY 987 CGATAAGGGGAGAGCTTGCAGGAGCGTTTATCAGCAACGACAAACAGCGCTATTCGGTGT 1046
Db 1209 ACCAAACGCGAGGAGCTGCGAGTAAATTCCTAACCGATGACAAACAACTCTTTGGTGT 1268
QY 1047 ATTCGAGGCAACAAATAG 1067
Db 1269 CTTTGGTGCTAAACAAGAGAG 1289

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
; US-08-232-463-14
Query Match 3.8%; Score 78.2; DB 1; Length 7218;
Best Local Similarity 5.7%; Pred. No. 3.7e-10;
Matches 23; Conservative 237; Mismatches 145; Indels 0; Gaps 0;
QY 1174 GATTTTGGTCATCCCGACAAACTTCTGTGCGAGGCAATCAAAATCTCTTTGGTTAGCCAA 1233
Db 1445 GAATTTGGTACRR 1386
QY 1234 GAGAAACCATCGAGCTTGCCGACGCGAGAAATGACCGTCAGTGTCTTTCGCACTTT 1293
Db 1385 RRR 1326
QY 1294 TTGACCTATGTAACTCGGACGGATAAAACCGAACCGCCCGCCGCAACCGAAGCG 1353
Db 1325 RRR 1266
QY 1354 CAGGACGAAGAGATTTCGGACATTGATAATGGCGAAGAAAGCGAAGCAAAATCGCGAT 1413
Db 1265 RRR 1206
QY 1414 GAAGAAAGAGCGACCGAAGATGACCGCGAGGAGATGAAGCGCAGCGAAGACGAGCC 1473
Db 1205 RRR 1146
QY 1474 ACAGAAACGAAGCGCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1533
Db 1145 RRR 1086
QY 1534 GAAGCAAGCGAGTTCAAAACGCCCTCTGCTGCTCCCGGAGCC 1578
Db 1085 RRR 1041
RESULT 3
US-09-059-584-45
; Sequence 45, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I

REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-794
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-059-584-45

Query Match 3.5%; Score 75.4; DB 4; Length 2121;
Best Local Similarity 48.2%; Pred. No. 1.1e-09;
Matches 251; Conservative 0; Mismatches 261; Indels 9; Gaps 1;

QY 747 TAAATATACGGTAGATTTCGGTAAACAAACCCCTGACGGGCGAGCTGATTAAAAACCAATA 806
Db 1008 TGAGTTTACTGTTAAATTTAAGGACAAAATTAACAGGTGAGCTGTTTAGTAACCTACA 1067
QY 807 TGTCAAAACCCAGTGAGAGCAAAACCGCTGACCATTTTACAACATCACTGCCGATTTAAA 866
Db 1068 AGACAGCGGTAAAGGCAATGTTACGAAACCAAAACGCTATGACATCGATGCCATATCTA 1127
QY 867 CGGCAACCGCTTTACCGGCGAGTGCACAGGTCAATCTGATTAGCGAAAGCCATGCCAA 926
Db 1128 CGGCAACCGCTTCGGTGGCAGTGCCACCGCAAGCGATAAAGCAAGCAAGCAAAACCAA 1187
QY 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGAGTTCGAGGCGGCTTTTTCGG 986
Db 1188 ACACCCC-----TTTACCAGCGATGCCAAATAGCTAGAGCGGCTTTTATGG 1238
QY 987 CGATAGGGGAGAGCTTCCGGAACGGTTTATCAGCAAGCAACAGCGGTATTCGGTGT 1046
Db 1239 ACCAAACCGCGAGGCTGGCAGGTAAATTCCTAACCAATGACAAACAACTCTTTGGCGT 1298
QY 1047 ATTCGAGGGCAAAACAAATAGCCCGTGGCTCTGGAAACACACCAAAATCTTGGATTC 1106
Db 1299 CTTTGGTGTAAACGAGAGAGTAAGCTGGGGGAAAAAACCAGAACCATCTTTAGATGCCA 1358
QY 1107 TCTGAAATTTCCGTTGATGAGGCAAGTGTTGAAATCCCGAGCGTTTGGCAATTTCTCC 1166
Db 1359 TGCATTTGGGACATTTAACAATAATACGCAACCACTTACCCTATTTACCAAAACA 1418
QY 1167 TATCCCGGATTTTGGTCAATCCGCAAACTTCTTGTGGAAGGCGATGAATTCCTTTGGT 1226
Db 1419 ACTGATAAATTTGGCAATGCCAAAGTTGGTCTTGGGTTCTACCGTCAATGATTGGT 1478
QY 1227 TAGCAAGAGAAACCATCGAGCTTGGCAGCGGAGNAAA 1267
Db 1479 GCCTACCGGTGTCACCAAGATGCAATGAATTCACCAAAA 1519

RESULT 4

US-08-778-570B-8
Sequence 8, Application US/08778570B
Patent No. 6437096
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario

RESULT 5

US-09-059-584-8
Sequence 8, Application US/09059584
Patent No. 6440701
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto

COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570B
FILING DATE: 03-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-664
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-778-570B-8

Query Match 3.5%; Score 75.4; DB 4; Length 2127;
Best Local Similarity 54.8%; Pred. No. 1.1e-09;
Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

QY 747 TAAATATACGGTAGATTTCGGTAAACAAACCCCTGACGGGCGAGCTGATTAAAAACCAATA 806
Db 1011 TGAGTTTACGGTAGATTTTTAGTAAAAAGAGCTAAAGAGTGAGCTGCTAGTAACATACA 1070
QY 807 TGTCAAAACCCAGTGAGAGCAAAACCGCTGACCATTTACAACATCACTGCCGATTTAAA 866
Db 1071 AGACGGCATAAAGGCGAGTGTTAATAAACCAACCGCTATGACATCGATGCCATATCTA 1130
QY 867 CGGCAACCGCTTTTACCGGCGAGTGCACAGGTCAATCTGATTAGCGAAAGCCATGCCAA 926
Db 1131 CGGCAACCGCTTTCGGTGGCAGTGCCACCGGAGCGATACACAGCAAGCAAGCA 1190
QY 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGATCAGCGCTTCCAGGCGCTTTCGG 986
Db 1191 ACACCCC-----TTTACCAGCGATGCCAAATAGCTAGAGCGGCTTTTATGG 1241
QY 987 CGATAGGGGGAAGAGCTTGCAGACCGTTTATCAGCAACGACACAGCGTATTCGGTGT 1046
Db 1242 ACCAAACCGCGAGGAGCTGGCAGGTAATTCCTAACCAATGACAAACAACTCTTTGGCGT 1301
QY 1047 ATTCGAGGCAACCAAAATAG 1067
Db 1302 CTTTGGTGTAAACGAGAG 1322

STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,584
FILING DATE: 14-APR-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-059-584-8

Query Match 3.5%; Score 75.4; DB 4; Length 2127;
Best Local Similarity 54.8%; Pred. No. 1.1e-09;
Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

QY 747 TAAATATACGGTAGATTTTCGGTAAACAAACCCCTGACGGCGAGCTGATTAATAAACCAATA 806
Db 1011 TGAGTTTACGGTAGATTTTAGTAAAGAGCCCTAAAGGTGAGCTGTCTAGTAACATACA 1070
QY 807 TGTCAAAACCCAGTGAAGCAAAAAACCGCTGACCATTTTACACATCACTGCCGATTTAAA 866
Db 1071 AGACGGCCATAGAGCGAGCTGTTTAAATAAACCAACGCTATGATGATGCCAATATCTA 1130
QY 867 CGGCAACCGCTTTACCGGAGTGCAGAGTCAATCTGATTTAGCGAAAGCCATGCCAA 926
Db 1131 CGGCAACCGCTTTCCGTGGCAGTGCACCGCAAGCGATACAACAGAGCAAGCAAAAGCAA 1190
QY 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGATCAGCGGCTTGAAGGCGGTTTTTCGG 986
Db 1191 ACACCCC-----TTTACCGAGTGCCTAAATAATAGCCCTAGAGGCGGTTTTATGG 1241
QY 987 CGATAAGGGGAAGAGCTTTCGGACGCTTTATCAGCAACGACCAACAGCGTATTCGGTGT 1046
Db 1242 ACCAAACCGCGAGAGCTGGCAGGTAAATTCCTAACCAATGACAACAACCTTTGGGT 1301
QY 1047 ATTGCAGGCAACAAATAG 1067
Db 1302 CTTTGGTCTAAACGAGAG 1322

RESULT 6

US-08-778-570B-7
Sequence 7, Application US/08778570B
Patent No. 6437096
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570B
FILING DATE: 03-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-664
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-778-570B-7

Query Match 3.5%; Score 75.4; DB 4; Length 3435;
Best Local Similarity 54.8%; Pred. No. 1.4e-09;
Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

QY 747 TAAATATACGGTAGATTTTCGGTAAACAAACCCCTGACGGCGAGCTGATTAATAAACCAATA 806
Db 1703 TGAGTTTACGGTAGATTTTAGTAAAGAGCCCTAAAGGTGAGCTGTCTAGTAACATACA 1762
QY 807 TGTCAAAACCCAGTGAAGCAAAAAACCGCTGACCATTTTACACATCACTGCCGATTTAAA 866
Db 1763 AGACGGCCATAGAGCGAGCTGTTTAAATAAACCAACGCTATGATGATGCCAATATCTA 1822
QY 867 CGGCAACCGCTTTACCGGAGTGCAGAGTCAATCTGATTTAGCGAAAGCCATGCCAA 926
Db 1823 CGGCAACCGCTTTCCGTGGCAGTGCACCGCAAGCGATACAACAGAGCAAGCAAAAGCAA 1882
QY 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGATCAGCGGCTTGAAGGCGGTTTTTCGG 986
Db 1883 ACACCCC-----TTTACCGAGTGCCTAAATAATAGCCCTAGAGGCGGTTTTATGG 1933
QY 987 CGATAAGGGGAAGAGCTTTCGGACGCTTTATCAGCAACGACCAACAGCGTATTCGGTGT 1046
Db 1934 ACCAAACCGCGAGAGCTGGCAGGTAAATTCCTAACCAATGACAACAACCTTTGGGT 1993
QY 1047 ATTGCAGGCAACAAATAG 1067
Db 1994 CTTTGGTCTAAACGAGAG 2014

RESULT 7

US-09-059-584-7
Sequence 7, Application US/09059584
Patent No. 6440701
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H

```
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 3435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-7

Query Match 3.5%; Score 75.4; DB 4; Length 3435;
Best Local Similarity 54.8%; Pred. No. 1.4e-09;
Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

Qy 747 TAAATATACGCTAGATTTCGGTAAACAAACCCCTGACGGCGAGCTGATTAAAAACCAATA 806
Db 1703 TGAGTTTACGCTAGATTTTAGTAAAGAGCCCTAAAGGTGAGCTGTCTAGTAACATACA 1762
Qy 807 TGTCAAACCCAGTGAGAGCAACAAACCCGCTGACCATTTACACATCACTGCCGATTTAAA 866
Db 1763 AGACGGCCATAAGGCGAGTGTAAATAAAACCAACGCTATGACATCGATGCGCAATATCTA 1822
Qy 867 CGGCAACCGCTTTACCGCGAGTGCCAGGTCAATCTGATTTAGCGAAAGCCATGCCAA 926
Db 1823 CGGCAACCGCTTCCGTGGCGAGTGCCAGGTCAATCTGATTTAGCGAAAGCCATGCCAA 1882
Qy 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGG 986
Db 1883 ACACCCC-----TTTACGAGGATGCCAAATAGCCTAGAGGGGTTTTTATGG 1933
Qy 987 CGATAAGGGGAGAGCTTGCGGAGCGGTTTATCAGAACGACAAACAGCGTATTCGGTGT 1046
Db 1934 ACCAAACCGGAGGAGCTGGCAGGTAAATTCCTAACCAATGACACAAACACTCTTTGGCGT 1993
Qy 1047 ATTCGAGGCAACAAATAG 1067
Db 1994 CTTTGGTGCTAACAGAGAG 2014

RESULT 8
US-08-448-194-7
; Sequence 7, Application US/08448194
; Patent No. 6028049
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; APPLICANT: LEBRAIN, Michele
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QY 1721 AAGAACGG-----CAAAAGCAGTATTTACCGTGTATTTCCGCAAGAAATCGATTTCCG 1774
| | | | |
Db 1810 AATAAGAGCGCGCAACAGGGCGGAATTTACTGTGAATTTGCGGATAAAAAATTTACCG 1869
| | | | |
QY 1775 GAACGCTGACGGAGAAAAAGGTGTAGAACCTCTTCCGTATTTGAAACGGCGGTGATTG 1834
| | | | |
Db 1870 GCAAGTTTAAACGCTGAAACAGCAGCGCGCAAACTTTTACCAATGAG---GGAATGATTC 1926
| | | | |
QY 1835 AGGCAACGCTTTCCATCGACAGCGCGCACTCGGATGACGGCATCGACTTTCGGGC 1894
| | | | |
Db 1927 AGGCAACGCTTTGAGGTACGCGCAAACTCTGAGTCAGTTTTGTATCTCGATCAAA 1886
| | | | |
QY 1895 AGGTTTCGACCAACCGCGAGATCTTCAAGCTAATGATCTTCTGTAGAGGAGGATTTT 1954
| | | | |
Db 1987 AATAACCAACCGCGCACTTAAAGCATATATACAGATGCAAGGTAAAGGGCGGTTTTT 2046
| | | | |
QY 1955 AGGCGCGAGGCGGAGGAATTTGGCGGTATTTTCAATATGATGGGAAA 2007
| | | | |
Db 2047 ACGGCGCTAAAGCGGAGAGTTGGCGGATGTTTGCCTATCCGCGCGATAAA 2099
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RESULT 9

US-08-867-921-7
; Sequence 7, Application US/08867921
; Patent No. 6326350
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; APPLICANT: LEGRAIN, Michele
; APPLICANT: MAZARIN, Veronique
; APPLICANT: BOUCHON-THEISEN, Bernadette
; APPLICANT: SCHRYVERS, Anthony B.
; APPLICANT: BLOCH, Marie-Aline
; TITLE OF INVENTION: DNA FRAGMENTS CODING FOR THE TRANSFERRIN
; RECEPTOR OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,921
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/445,472
; FILING DATE: 22-MAY-1995
; APPLICATION NUMBER: US 08/361,469
; FILING DATE: 22-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,053
; FILING DATE: 18-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92 07493
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

LENGTH: 2230 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: DNA which encodes Tbp2 subunit of transferrin
ORGANISM: Neisseria meningitidis IM2169
STRAIN: Neisseria meningitidis IM2169
FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 60..119
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 120..2192
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..2192
; US-08-867-921-7

Query Match 3.3%; Score 71; DB 4; Length 2230;
Best Local Similarity 51.8%; Pred. No. 1.5e-08;
Matches 214; Conservative 0; Mismatches 190; Indels 9; Gaps 2;
QY 1601 TTTTCTGAAAGTATCCGACGCGCAGAAACGAAATATTCGCAAACTGGGAGAAAGCAGCT 1660
| | | | |
Db 1690 TGTTCCTCCAAGGCGAGCGTACCGATGAAAAAGAGATTCCAAACCGACCAAAACGTCGTTT 1749
| | | | |
QY 1661 ATACCGGCACTTGGGAGCGCGTATCGGCAAAACCCATTTCAATGGGCAATCATGCGGATA 1720
| | | | |
Db 1750 ATCGGGGGTCTTGGTACGGGCGATATTCGCAACGGCAAGCTGGAGCGCAATGCTTCTG 1809
| | | | |
QY 1721 AAGAAGCGG-----CAAAAGCAGTATTTTACCGTTCGATTTTCGGCAAGAAATCGATTTCCG 1774
| | | | |
Db 1810 AATAAGAGGCGGCAACAGGCGGAAATTTACTGTGAATTTTCCGATATAAAAAATTTACCG 1869
| | | | |
QY 1775 GAACGCTGACGGAGAAAAACGGTGTAGAACCTCTTTCGTTTCGTTATTTGAAAAACGGCGTATTG 1834
| | | | |
Db 1870 GCAAGTTTAAACGCTGAAACAGCGAGCGCGCAAACTTTTACCATTGAG---GGAATGATTC 1926
| | | | |
QY 1835 AGGCAACGCTTTCCATCGACAGCGCGCACTCGGATGACGGCATCGACCTTTCGGGC 1894
| | | | |
Db 1927 AGGCAACGCTTTGAGGTACGCGCAAACTCTGAGTCAGTTTTGTATCTCGATCAAA 1886
| | | | |
QY 1895 AGGTTTCGACCAACCGCGAGATCTTCAAGCTAATGATCTTCTGTAGAGGAGGATTTT 1954
| | | | |
Db 1987 AATAACCAACCGCGCACTTAAAGCATATATACAGATGCAAGGTAAAGGGCGGTTTTT 2046
| | | | |
QY 1955 ACGGCGCGAAGCGCGGAGGAAATTTGGCGGTATTTTCAATATGATGGGAAA 2007
| | | | |
Db 2047 ACGGCGCTAAAGCGGAGAGTTGGCGGATGTTTGCCTATCCGCGCGATAAA 2099
| | | | |

RESULT 10

US-09-059-584-48
; Sequence 48, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada

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; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-48

Query Match          3.3%; Score 70.8; DB 4; Length 2145;
Best Local Similarity 54.1%; Pred. No. 1.7e-08;
Matches 172; Conservative 0; Mismatches 137; Indels 9; Gaps 1;

QY 747 TAATATACGGTAGATTTCGGTACAAAACCCCTGACGGGCGAGCTGATTTAAAAACCAATA 806
Db 1017 TGAATTACTGTTAATTAAAGGAAAAAAATTAACAGGTGAGCTGTTTAGTAACTTACA 1076

QY 807 TGTCAACCCAGTCAGAGCAAAAACCGCTGACCATTTTACACATCACTGCCGATTTAAA 866
Db 1077 AGACAGCCATAAACAAGTAACCAAAAACAAACCGCTATGATTAAGGCTGATATCCA 1136

QY 867 CGGCAACCGCTTTACCGGCAAGTCCAGGTCATCTGATTAGCGAAAAGCCATGCAAA 926
Db 1137 CGGCAACCGCTTCGTCGTCAGTCCACGCAACGGATAAGCAGACAGACAGCAAAAGCAA 1196

QY 927 TAAGGAGCATTTGTTTTCCATGCGCATGCGGCTTACGCGGCTTTCGAGGCGGTTTTTCGG 986
Db 1197 ACACCCC-----TTTACCAGCCATGCCAAAAGATAAGCTAGAAAGTGTTTTTATGG 1247

QY 987 CGATAAGGGGGAAGAGCTTGCAGGACGGTTTATCAGCAACGACACAGCGTATTCGGTGT 1046
Db 1248 ACCAAAAGGCGAGGAGCTGGCAGGTAAATCTTAACCGATGATACAAACTCTTTGGTGT 1307

QY 1047 ATTCGCGAGCAAAACAAA 1064
Db 1308 CTTTGGTGCCAAACAAGA 1325

RESULT 11
US-09-059-584-47
; Sequence 47, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-47

Query Match          3.3%; Score 70.8; DB 4; Length 2287;
Best Local Similarity 54.1%; Pred. No. 1.7e-08;
Matches 172; Conservative 0; Mismatches 137; Indels 9; Gaps 1;

QY 747 TAATATACGGTAGATTTCGGTACAAAACCCCTGACGGGCGAGCTGATTTAAAAACCAATA 806
Db 1159 TGAATTACTGTTAATTAAAGGAAAAAAATTAACAGGTGAGCTGTTTAGTAACTTACA 1218

QY 807 TGTCAAAACCCAGTCAGAGCAAAAACCGCTGACCATTTTACAACTCACTGCCGATTTAAA 866
Db 1219 AGACAGCCATAAACAAGTAACCAAAAACAAACGCTATGATTAAGGCTGATATCCA 1278

QY 867 CGGCAACCGCTTTACCGGCAAGTCCAGGTCATCTGATTTAGCGAAAAGCCATGCAAA 926
Db 1279 CGGCAACCGCTTCGTCGTCAGTCCACGCAACGGATAAGGCAAGACAGCAAAAGCAA 1338

QY 927 TAAGGAGCATTTGTTTTCCATGCGCATGCGGCTTTCAGCGGCTTTCGAGGCGGTTTTTCGG 986
Db 1339 ACACCCC-----TTTACCAGCCATGCCAAAAGATAAGCTAGAAAGTGTTTTTATGG 1389

QY 987 CGATAAGGGGGAAGAGCTTGCAGGACGGTTTATCAGCAACGACACAGCGTATTCGGTGT 1046
Db 1390 ACCAAAAGGCGAGGAGCTGGCAGGTAAATCTTAAACCGATGATACAAACTCTTTGGTGT 1449

QY 1047 ATTCGCGAGCAAAACAAA 1064
Db 1450 CTTTGGTGCCAAACAAGA 1467

RESULT 12
US-09-596-002-30
; Sequence 30, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Legace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US

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RESULT 13
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:

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RESULT 14
US-09-671-317-439/c
: Sequence 439, Application US/09671317
: Patent No. 6528260
: GENERAL INFORMATION:
: APPLICANT: Blumenfeld, Marta
: APPLICANT: Chumakov, Ilya
: APPLICANT: Bougueleret, Lydie
: APPLICANT: Cohen, Annick
: TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
: FILE REFERENCE: 62.US3.CIP
: CURRENT APPLICATION NUMBER: US/09/671,317
: CURRENT FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: US 09/536,178
: PRIOR FILING DATE: 2000-03-23
: PRIOR APPLICATION NUMBER: PCT/IB00/00403
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: US 60/126,269
: PRIOR FILING DATE: 1999-03-25
: PRIOR APPLICATION NUMBER: US 60/131,961
: PRIOR FILING DATE: 1999-04-30
: NUMBER OF SEQ ID NOS: 977
: SOFTWARE: Patent.pm
: SEQ ID NO 439
: LENGTH: 1001
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: allele

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LOCATION: 501
OTHER INFORMATION: 12-454-242 : deletion AT
NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 12-454-242.misl, potential
NAME/KEY: primer_bind
LOCATION: 260..279
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 755..773
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_feature
LOCATION: 795..800
OTHER INFORMATION: n=a, g, c or t
US-09-671-317-439

Query Match 3.2%; Score 69.2; DB 4; Length 1001;
Best Local Similarity 62.6%; Pred. No. 3e-08;
Matches 124; Conservative 0; Mismatches 73; Indels 1; Gaps 1;

QY 1341 CAACCGAAGCGGAGGAGGATTCGGACATTGATGTCGCGAAGAAAGCGAAGA 1400
Db 1001 CCATCTCAAG 942
QY 1401 CGAATCGCGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1460
Db 941 AGAAG 882
QY 1461 AGAAG 1519
Db 881 AGAAG 822
QY 1520 AAGATCGTCGCGAGAG 1537
Db 821 AAGAAGAGAGAGAGAGAG 804

RESULT 15
US-09-197-649-7
Sequence 7, Application US/09197649
Patent No. 6194550
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Pribnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match 3.1%; Score 67.6; DB 3; Length 390;
Best Local Similarity 55.6%; Pred. No. 4.8e-08;
Matches 130; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 1326 CGAAGCGCGCGCCCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1385

Db 140 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 199
QY 1386 CGAAGAAAGCGAAGACGAAATCGGCGATGAAGAAGAGGACCGAAAGATGCGAGCGGAGG 1445
Db 200 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 259
QY 1446 AGATGAAGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1505
Db 260 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 319
QY 1506 TGAAGAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1559
Db 320 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 373

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 22:06:19 ; Search time 965 Seconds

(without alignments)
11071.388 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3228839 seqs, 2456066551 residues

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1487.2	68.4	2226	17	US-10-735-098-5, Appli
3	1462.2	67.2	2262	17	US-10-735-098-7, Appli
4	1454.8	66.9	2226	13	US-10-282-122A-29815
5	1304.8	60.0	2169	17	US-10-735-098-3
6	1296.2	59.6	2124	17	US-10-735-098-9
7	678.6	31.2	1000	17	US-10-343-561-15
8	174.2	8.0	3300	17	US-10-467-534-80
9	81.6	3.8	31124	13	US-10-087-192-463
10	80.2	3.7	374949	13	US-10-087-192-1627
11	79.4	3.7	54786	12	US-10-052-482-211
12	78.2	3.6	635	13	US-10-027-632-269927
13	78.2	3.6	635	16	US-10-027-632-269927
14	78	3.6	305	9	US-09-864-761-19262

c 15 78 3.6 496 9 US-09-864-761-2534
c 16 75.6 3.5 276 9 US-09-864-761-20595
c 17 75.6 3.5 193853 13 US-10-087-192-1663
c 18 75 3.4 37265 13 US-10-087-192-49
c 19 73.6 3.4 554 14 US-10-101-487-69
c 20 73.6 3.4 554 14 US-10-101-487-106
c 21 73.4 3.4 96596 12 US-10-052-482-70
c 22 72.8 3.3 39443 16 US-10-085-117-313
c 23 72.2 3.3 522 14 US-10-101-487-71
c 24 72.2 3.3 530 14 US-10-101-487-73
c 25 72.2 3.3 122859 13 US-10-087-192-37
c 26 72 3.3 2052 17 US-10-467-534-85
c 27 71.4 3.3 511 13 US-10-027-632-302235
c 28 71.4 3.3 511 16 US-10-027-632-302235
c 29 71.4 3.3 927 16 US-10-369-493-26106
c 30 71.4 3.3 1032 16 US-10-369-493-26107
c 31 71.4 3.3 48652 13 US-10-087-192-859
c 32 71.2 3.3 462 9 US-09-864-761-3829
c 33 71 3.3 536 15 US-10-029-386-19974
c 34 71 3.3 599 15 US-10-029-386-6243
c 35 71 3.3 2232 15 US-10-087-464-45
c 36 70.8 3.3 58909 13 US-10-672-787-30
c 37 70.6 3.2 49753 13 US-10-087-192-1855
c 38 70.4 3.2 96597 12 US-10-052-482-103
c 39 69.6 3.2 33454 13 US-10-087-192-1111
c 40 69.6 3.2 96595 12 US-09-997-722-43
c 41 69.4 3.2 438 9 US-09-864-761-4988
c 42 69.4 3.2 32069 15 US-10-004-113-7
c 43 69.4 3.2 202251 13 US-10-087-192-985
c 44 69.2 3.2 929 13 US-10-294-934-14
c 45 69.2 3.2 1001 13 US-10-294-934-439

ALIGNMENTS

RESULT 1

US-10-735-098-1
; Sequence 1, Application US/10735098
; Publication NO. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tomassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 1
; LENGTH: 2277
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain BNCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(2274)
US-10-735-098-1

Query Match 100.0%; Score 2175; DB 17; Length 2277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTAACCGAATTATGGCGGCATGTCTTTGTCCTTACTTTTGGCATCTTGTATC 60
DB 100 ATGTGTAACCGAATTATGGCGGCATGTCTTTGTCCTTACTTTTGGCATCTTGTATC 159

applicants

QY	61	GGCGCAATTTTCGGCGTGGAGCTGTGTTGCGAATCAACGCCGACCGCGTACCCCGTCACT	120
DB	160	GGCGCAATTTTCGGCGTGGAGCTGTGTTGCGAATCAACGCCGACCGCGTACCCCGTCACT	219
QY	121	TTCAAGTCTAAGGACGTTCCGCATCCCGCCCTCGCCCAACCTTCTATAGAAATCACCGG	180
DB	220	TTCAAGTCTAAGGACGTTCCCATCCCGCCCTCGCCCAACCTTCTATAGAAATCACCGG	279
QY	181	GTCAAACCGGCCCGCGTCGGTCGGCAATGCGGCTGCCAAGCGGAATACTGCTTTTCAT	240
DB	280	GTCAAACCGGCCCGCGTCGGTCGGCAATGCGGCTGCCAAGCGGAATACTGCTTTTCAT	339
QY	241	CGTGAAGATGGCACGGAAATTCCAAATAGCAAAACGAGCAAGAAAAGCTGCTGTTTCAA	300
DB	340	CGTGAAGATGGCACGGAAATTCCAAATAGCAAAACGAGCAAGAAAAGCTGCTGTTTCAA	399
QY	301	GAAGTGATGTTCTGTTTTATACGGTTTCAAAAGGAAATAAATCTCAACAATCTTAAAGC	360
DB	400	GAAGTGATGTTCTGTTTTATACGGTTTCAAAAGGAAATAAATCTCAACAATCTTAAAGC	459
QY	361	GAATTCATAAACCGTGATTCGCGATGTAGAAATTAGCAATCAGAAAAGGAAAAATAAAAA	420
DB	460	GAATTCATAAACCGTGATTCGCGATGTAGAAATTAGCAATCAGAAAAGGAAAAATAAAAA	519
QY	421	TATGATTTAAATTTGTAGATGCGAGTTATGTTATATGTTAAAGGAAAAGATGAAATTAAAG	480
DB	520	TATGATTTAAATTTGTAGATGCGAGTTATGTTATGTTAAAGGAAAAGATGAAATTAAAG	579
QY	481	TGGACTTCAGATTAACAAGCAGTTTCCAAACCGCTTAGGTATGACGGTTTGTATATTAT	540
DB	580	TGGACTTCAGATTAACAAGCAGTTTCCAAACCGCTTAGGTATGACGGTTTGTATATTAT	639
QY	541	TCGGAGAACGTCCTTCCCAATCTTTACCGAGTCGGGAACGGTGGAAATATCTGGTAAC	600
DB	640	TCGGAGAACGTCCTTCCCAATCTTTACCGAGTCGGGAACGGTGGAAATATCTGGTAAC	699
QY	601	TGGCAATATATGACCGATGCCAAACGTCATCAGCAGTAAGGCGGTTGGCAATTGCAAT	660
DB	700	TGGCAATATATGACCGATGCCAAACGTCATCAGCAGTAAGGCGGTTGGCAATTGCAAT	759
QY	661	TTGGGTTATTACACATTTTATGTTAAACGATGCGTGCAACTTCTATGCGGCTAAGCAT	720
DB	760	TTGGGTTATTACACATTTTATGTTAAACGATGCGTGCAACTTCTATGCGGCTAAGCAT	819
QY	721	GTCCAGAAAGGAAAAACAFTCTGCTAAATATACGCTAGATTTCCGTTAACAAACCCCTG	780
DB	820	GTCCAGAAAGGAAAAACAFTCTGCTAAATATACGCTAGATTTCCGTTAACAAACCCCTG	879
QY	781	ACGGCGAGCTGATTAAACCAATATGTCAAAACCGAGTGAGAGCAAAAACCGCTGACC	840
DB	880	ACGGCGAGCTGATTAAACCAATATGTCAAAACCGAGTGAGAGCAAAAACCGCTGACC	939
QY	841	ATTTTAACACATCACTGCGGATTTTAAAACGGCAACCGCTTTACCGGCAGTGCCCAAGTCAAT	900
DB	940	ATTTTAACACATCACTGCGGATTTTAAAACGGCAACCGCTTTACCGGCAGTGCCCAAGTCAAT	999
QY	901	CCTGATTTAGGAAAAACGATGCCAATAGGAGCATTTGTTTTTCCATGCCGATGCCGAT	960
DB	1000	CCTGATTTAGGAAAAACGATGCCAATAGGAGCATTTGTTTTTCCATGCCGATGCCGAT	1059
QY	961	CAGCGGCTTGAGGCGGTTTTTTTCGGCGATAGGGGAAAGCTTGCAGACGTTTTATC	1020
DB	1060	CAGCGGCTTGAGGCGGTTTTTTTCGGCGATAGGGGAAAGCTTGCAGACGTTTTATC	1119
QY	1021	AGCAACGACAAACACGCTATTCCGTTGTTATCCGAGGCAAAAATAATAGCCCGCTCT	1080
DB	1120	AGCAACGACAAACACGCTATTCCGTTGTTATCCGAGGCAAAAATAATAGCCCGCTCT	1179
QY	1081	GGAAAAACACCAAAATCTTGGATTTCTGAAAAATTTCCGTTGATGAGGCAAGTGGTAA	1140
DB	1180	GGAAAAACACCAAAATCTTGGATTTCTGAAAAATTTCCGTTGATGAGGCAAGTGGTAA	1239

QY	1141	AATCCCGACCGTTTGGCAATTTCTCTATGCCCAGATTTTGGTCAATCCCGACAAACTTCTT	1200
DB	1240	AATCCCGACCGTTTGGCAATTTCTCTATGCCCAGATTTTGGTCAATCCCGACAAACTTCTT	1299
QY	1201	GTCCGAAGCGCATGAAATTCCTTTGGTTAGCCAGAGAAAACCATCGAGCTTCCGACGGC	1260
DB	1300	GTCCGAAGCGCATGAAATTCCTTTGGTTAGCCAGAGAAAACCATCGAGCTTCCGACGGC	1359
QY	1261	AGGAAATGACCGCTAGTGTCTGTGCGACTTTTGTACCTATGTGAAATCGGACGGATA	1320
DB	1360	AGGAAATGACCGCTAGTGTCTGTGCGACTTTTGTACCTATGTGAAATCGGACGGATA	1419
QY	1321	AAAACCGAACGCCCGCCGCAACCGAAGCGCCAGGACGAAGACGATTCGGACATGTGAT	1380
DB	1420	AAAACCGAAACGCCCGCCGCAACCGAAGCGCCAGGACGAAGACGATTCGGACATGTGAT	1479
QY	1381	AATGGCGAAAGAACGGAAGCAAAATCGGCGATGAAGAGAACGCCACCGAAGATCGAGC	1440
DB	1480	AATGGCGAAAGAACGGAAGCAAAATCGGCGATGAAGAGAACGCCACCGAAGATCGAGC	1539
QY	1441	GCAGGAGATGAAGCGCAGGAAGACGAAGACCAAGCAAGAAACGAAGCGCGGAAGAC	1500
DB	1540	GCAGGAGATGAAGCGCAGGAAGACGAAGACCAAGCAAGAAACGAAGCGCGGAAGAC	1599
QY	1501	GAAGCTCAAGAACTGTGAAGAAAGAAATCGTGGCGAAGAGGCAACCGCAGTTCAAACGCCATC	1560
DB	1600	GAAGCTCAAGAACTGTGAAGAAAGAAATCGTGGCGAAGAGGCAACCGCAGTTCAAACGCCATC	1659
QY	1561	CTGCCTGTCCGGAAGCCTCTAAAGGCGAGGATATCGACCTTTTCTGAAAGTATCCGC	1620
DB	1660	CTGCCTGTCCGGAAGCCTCTAAAGGCGAGGATATCGACCTTTTCTGAAAGTATCCGC	1719
QY	1621	ACGCGCAAGACGATATTCGCAAACTGGAGAGACGCTATACCGGCACTTTGGGAGCG	1680
DB	1720	ACGCGCAAGACGATATTCGCAAACTGGAGAGACGCTATACCGGCACTTTGGGAGCG	1779
QY	1681	CGTATCGGCAAAACCCATTCAATGGGCAAAATCATCGCGATAAAGAACGGCGAAAGCAGTA	1740
DB	1780	CGTATCGGCAAAACCCATTCAATGGGCAAAATCATCGCGATAAAGAACGGCGAAAGCAGTA	1839
QY	1741	TTTACCGTTGATTTGGCAAGAAATCGATTTCCGGAACGCTGACGAGAGAAAACGGTGTA	1800
DB	1840	TTTACCGTTGATTTGGCAAGAAATCGATTTCCGGAACGCTGACGAGAGAAAACGGTGTA	1899
QY	1801	GAACCTGCTTTTCGTTATGAAAACGCGCTGATTGAGGCAACGGTTTCCATGCGACAGCG	1860
DB	1900	GAACCTGCTTTTCGTTATGAAAACGCGCGTGAATTGAGGCGCAACGGTTTCCATGCGACAGCG	1959
QY	1861	CGCACTCGGATGACCGCATCGACCTTTCCGCGCAGGTTCCGACCAACCGCAGATCTTC	1920
DB	1960	CGCACTCGGATGACCGCATCGACCTTTCCGCGCAGGTTCCGACCAACCGCAGATCTTC	2019
QY	1921	AAAGCTTAATGATCTTCGTTGTAAGAGAGGATTTTACGCCCGCAAGCGCGAGAAATGGCG	1980
DB	2020	AAAGCTTAATGATCTTCGTTGTAAGAGAGGATTTTACGCCCGCAAGCGCGAGAAATGGCG	2079
QY	1981	GGTATTATTTTCAATATGATGGGAAATCTCTGGGTATAACTGAAGTACTGAAATAAA	2040
DB	2080	GGTATTATTTTCAATATGATGGGAAATCTCTGGGTATAACTGAAGTACTGAAATAAA	2139
QY	2041	GTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAA	2100
DB	2140	GTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAA	2199
QY	2101	CAGTTAAACCTCAAGTTTAAACCCCAATTCGCGCTGGTATTCGGTSCGAAGAAAGATAAT	2160
DB	2200	CAGTTAAACCTCAAGTTTAAACCCCAATTCGCGCTGGTATTCGGTSCGAAGAAAGATAAT	2259
QY	2161	AAAGAGGTGAAAAA	2175
DB	2260	AAAGAGGTGAAAAA	2274

RESULT 2

US-10-735-098-5
; Sequence 5, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tomassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain H44/76
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2223)

US-10-735-098-5
Query Match 68.4%; Score 1487.2; DB 17; Length 2226;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 1856; Conservative 0; Mismatches 298; Indels 90; Gaps 10;

Qy	1	ATGTGTAACCGAATATGCGGCATTTCTTTGTTGCCCTTACTTTTGGCATCTTGTATC	60
Db	1	ATGTGTAACCGAATATGCGGCATTTCTTTGTTGCCCTTACTTTTGGCATCTTGTAT	60
Qy	61	GGCGCAATTTGGGGTGCAGCTTGTTCGAAATCAAGCGCGACCGGTACCCGTCAC	120
Db	61	GGCGCAATTTGGGGTGCAGCTTGTTCGAAATCAAGCGCGACCGGTACCCGTCAC	120
Qy	121	TTCAAGTCTAAGAGGTTCCCACTCGCGCCCTGCGCAAACTTCTATAGAAATCAGCGG	180
Db	121	TTCAAGTCTAAGAGGTTCCCACTCGCGCCCTGCGCAAACTTCTATAGAAATCAGCGG	180
Qy	181	GT-----CAACCGGCCCGCTCGGTGGCAATCGCGTCCCAAGCGGGAATCTGCT	234
Db	181	GTGCGGTCAACCGGCCCTGCGGTGGCAATCGCGTCTGTGAGGCGGATTTTCGCA	240
Qy	235	TTTCATCGTGAAGTGGACGGAAATTCGAATAGCAAAACAGCAAGAGAAAGCTGTG	294
Db	241	ACTTCTGATAGGTTGGCAATGATTTCCAAATAGCAAAACAGCAAGAGAAAGCTGTG	300
Qy	295	TTTCAAGAGGTGATGTTCTGTTTATACGGTTCAAAAGAGAAATAAACTTCAACAACT	354
Db	301	TTTAAAGAGGTGATGTTCTGTTTATACGGTTCAAAAGAGATAAACTTCAAGTGGCT	360
Qy	355	AAAAAGCAATTCATAAAGCTGATTCGGATGAGAAATTTAGACATTCAGAAAGGAAAT	414
Db	361	AAGGATAAATTCATCAACGCAATCTAATGTAGAAATTTAGGACATCAGAAATGAAAT	420
Qy	415	AAAAATATGATTAATAATTTGTAGATGAGGTTATGTATA-----TGTAAAGGAAAGAT	471
Db	421	AAAAATATGTTATGAAATTTGTGATGCGGTTATGTATATATACTAAAAACGGAACAGAT	480
Qy	472	GAAATTAAGTGACTTCAGATTCAGCAGTTTCCACCGCTTAGTTTATGACCGTTTT	531
Db	481	GAAATTAAGTGACTTCAGATTCAGCAGTTTCTTAATCGTTTGGTACGACGTTTT	540
Qy	532	GTATATATTTCGGGAAAGCTCTTCCCAATCTTTACCGAGTGGCGGAACGGTGAATAT	591
Db	541	GTATATATTTCGGGAAACATCTTCCCAATCTTTACCGAGCGGGAACGGTGCATAT	600

Qy	592	TCTGTTAACTGGCAATATATGACCGATGCCAAACGTTCATCGAGCAGGTAAGGC---	648
Db	601	TCCGTTAACTGGCAATATATGACCGATGCCAATCGTTCATCGAAAGGAAAGCAGGAGAT	660
Qy	649	GGCATTTGACAAATTTGGGTATTACACATTTTATCGTTAACGATGTTGGTGCACCTTTTAT	708
Db	661	CCTAGCGAAGATTTGGGTATTCTCGTTTATTACGGTCAAAATGTCGGAGCAACTTCTTAT	720
Qy	709	CGCGTTAAGATGTCGAGAAAGGAAACATCTGCTAAATATACGTTAGATTTCCGT	768
Db	721	GCTCGGACTGCCGACGACCGGAGGGAACATCTGCCGAATATACGGTTGATTTCCGAT	780
Qy	769	AACAAAACCTGACGGCGAGCTGATTAAAAACCAATATGT---CAAAACCCAGTGAGAAG	825
Db	781	AAGAAAACCTTTGACGGTCAATTAATTAATAATCAGTATGTGCAAAAGAAAACCGATGAA	840
Qy	826	CAAAAACCGTGCACATTTTCAACATCATCTCCGATTTAAACGGCAACCGTTTACCGGC	885
Db	841	AAGAAACCACTGACCATTTTACGACATTACGCAACATTTGGACGGCAACCGCTTTACCGC	900
Qy	886	AGTGCRAAGTCAATCTGATTTAGCGAAAGCCATGCCAATAGGAGCATTTGTTTTTC	945
Db	901	AGTGCRAAGTAAACCGAGTTGAAGACGAGCCACGCTGATAAAGAGCATTTGTTTTTC	960
Qy	946	CATGCCGATGCCGATCAGCGCTTGAGGGCGTTTTTTCGGCGATAAGGGGGAAGAGCTT	1005
Db	961	CATACCGATGCCGATCAGCGCTTGAGGGCGTTTTTTCGGCGATAAGGGGGAAGAGCTT	1020
Qy	1006	GCCGACGGTTTTATCAGCAACGACACGATTTGGGTATTTCGCGAGGCAACA-----	1061
Db	1021	GCCGACGGTTTTATCAGCAACGACACGATTTTCGGCGTATTCGCGAGCAAAAAACA	1080
Qy	1062	-----AAATAGCCCGTCCGCTCTGGAACACACACCAAAATC	1098
Db	1081	AACGCATCAAAACGACGAGATACAAATCTGATGCGCTCTGAAAAACACACCAAAATC	1140
Qy	1099	TTGATTTCTTGAAATTTCCGTTGATGAGCAAGTGGTGAATAATCCCGACCGTTTGC	1158
Db	1141	TTGATTTCTTGAAATTTCCGTTGACGAGCGCGGATATAAATGCCCGCGTTTGC	1200
Qy	1159	ATTTCTCTATGCCGATTTTGGTTCATCCGCAAACTTTCTTGTGCAAGGGGATGAAAT	1218
Db	1201	ATTTCCCTCTGCCGATTTTGGCATCCGCAAACTCTTGTGCAAGGGGCTGAAAT	1260
Qy	1219	CTTTGGTTAGCAGAAACCATCGAGCTGCGGACGCGAGGAAATGACCGTCACT	1278
Db	1261	CTTTGGTTAGCAGAAACCATCGAGCTTGCAGCGGAGGAAATGACCGTCACT	1320
Qy	1279	GCTTCTCGCATTTTTCACCTATGTGAACTTCGGACGGATAAAAAACCGAACCGCCGCC	1338
Db	1321	GCTTGTTCGATTTTCTGACCTATGTGAACTTCGACGGATACAGGCTTGTGTAACGAC	1380
Qy	1339	GCAAAACCGAAGGC-----GCAGACGAAGAGGATTCGGAATTTGATTAATGGC	1386
Db	1381	AGTAAACCAAGGCGGAAGATAAGGGAAGGATGAAGAGGATACAGGCTTGTGTAACGAC	1440
Qy	1387	GAAGAAAGC---GAAGACGAATCGGCGATGAAGAGGAGCAGCGAGAGATCGACCGCA	1443
Db	1441	GAAGAAAGCAGGAAGATGAAGCGCGACGAGGAGGCGGAAGCGGAATCGGCTCGG	1500
Qy	1444	GGAGATGAAGGCGAGGAAGACGAAGCCACAGAAAAACGAAGACGGCGGAAGACGAA	1503
Db	1501	GATGAAGAGGAGGTTGCGAGACGAGCCGCAAGAAACGAAGGCGGCGGAAGACGAA	1560
Qy	1504	GCTGAAGAACCT-----GAAGAAGATCTGTCGGCAGAAAGCAAC---GGCAGTTCA	1551
Db	1561	GCTGAAGAACCTGAAGAACCCGGAAGAAATCGCGCGAGAAAGCGCGGCTGTTGTTCA	1620
Qy	1552	AACGCCATCTCGCTGTCGCGAAGCCTTAAGGACGGGATATCGACCTTTCTCTGAA	1611
Db	1621	GACGGCATCTCGCTGTCGCGAAGCTCTTAAGGACGGGATATCGACCTTTCTCTGAA	1680

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QY 1612 GGTATCGCACGGCAGAAAAGAAATATTCGCAAACTGGAGAAGCACGCTATACCGCACT 1671
Db 1681 GGTATCGCACGGCGGAGCGGACATTCGCAAACTGGAAAAGCACGCTATACCGCACT 1740
QY 1672 TGGGAAGCGCGTATCGGCAAAACCAATTCATATGGGCAATCATGCGGATAAAGAGCGCA 1731
Db 1741 TGGGAAGCGCGTATCAGCAAAACCAATTCATATGGGCAATCATGCGGATAAAGAGCGCA 1800
QY 1732 AAAGCAGTATTTACCGTTGATTTTCGCAAGAAATCGAATTCGCGAAGCTGACGGAGAAA 1791
Db 1801 AAAGCAGATTTGACGTTGATTTTCGCGGAGAAATCGAATTTCCGGAAGCGCTGACGGAGAAA 1860
QY 1792 AACGGTGTAGAACCTGCTTTCCGTATTTGAAAACGGCGTGATTCAGGGCAACGGTTTCCAT 1851
Db 1861 AACGGTGTACAACTGCTTTCCCATATTTGAAAACGGCGTGATTCAGGGCAATGGTTTCCAC 1920
QY 1852 GCGACACGGCGCACTCGGAGTAGCGGATCGACCTTTTCGGGGCAGGGTTTCGACCAAAACCG 1911
Db 1921 GCGACACGGCGCACTCGGGATAACGGCATCAATCTTTTCGGGAAATGATTCGACTAATCCT 1980
QY 1912 CAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGAGGATTTTACGCGCCGGAAGCGGAG 1971
Db 1981 CCAAGTTTCAAGCCAAATATCTCTGTGAACAGGCGCTTTTACGCGCCGCGAGCGGAG 2040
QY 1972 GAATTCGGCGGTATATTTTCAATAATGATGGGAAATCTCTTGGTATAACTGAAGGTACT 2031
Db 2041 GAATTCGGCGGTACTATTTTCAATAATGATGGGAAATCTCTTGGTATAACTGAAGTACT 2100
QY 2032 GAAATTAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2091
Db 2101 GAAATTAAGCTGAAGCTGAAGTTGAAAATGAAAGCTGGTGT----- 2141
QY 2092 GATGTTGAACAGTTAAACCTGAAAGTTTAAACCCCAATTCGGCGTGGTATTCGGTGGGAAG 2151
Db 2142 --TGGCAACAGTTAAACCTGAAGCTTAAACCCCAATTCGGCGTGGTATTCGGTGGGAAG 2199
QY 2152 AAAGATAATAAGAGGTGGAAAAA 2175
Db 2200 AAAGATAATAAGAGGTGGAAAAA 2223
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RESULT 3

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US-10-735-098-7
; Sequence 7, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M990
; FEATURE:
; LOCATION: (1) ... (2259)
US-10-735-098-7
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Query Match 67.2%; Score 1462.2; DB 17; Length 2262;
Best Local Similarity 81.1%; Pred. No. 0;

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Matches 1832; Conservative 0; Mismatches 343; Indels 84; Gaps 8;
QY 1 ATGTGTAACCGAAATTAATGCGCGGCAATTTGCTTGTGCGCTTACTTTTGGCAATCTTGTATC 60
Db 1 ATGTGTAACCGAAATTAATGCGCGGCAATTTGCTTGTGCGCTTACTTTTGGCAATCTTGTATC 60
QY 61 GCGCGCAATTTTCGCGTGCAGCTGTTGTCGAATCAACGCGCACCGCG----- 108
Db 61 GCGCGCAATTTTCGCGGTAACAGCTGTTGTCGAATCAACGCGCACCGCGCAACTCTGTCTCA 120
QY 109 TACCCCGTCACTTTCAGTCTAAGGACGTTCCCACTCCGCGCCCTGTCACCAACCTTCTATA 169
Db 121 GATTCAAAATCTTCCAAATCTCGCGGATAAGCTCTCCAGCTCCTCGCGAGCCTTCGGTA 180
QY 169 GAAATCAGCGCGGTCAACCGCGCGCGCTCGGTGCGGCAATGCGGTGCCAAGCGGAAT 228
Db 181 GAAATCAGCGCGGTCAAGCGCGCGCGCTCGGTGCGGCAATGCGGTGCCAAGCGGAAT 240
QY 229 ACTGCTTTTCATCGTCAAGATGGCAGGAAATTCCAAATAGCAAAACAAGCAGAGAAAAG 288
Db 241 ATCGCAACTTTTGTATATAAATGGTAATGAAATTCCTCAATAGTAAGCGGAGAGGAGTAT 300
QY 289 CTGCTGTTCAAGAAAGTGATGTTCTGTTTATACGGTTCAAAAGGAAATAAACTTCAA 348
Db 301 CTGCGCGTCAAGAGAGGATATCTCTGTTTATAGACGCTACGCGCAAGAACAGGCTGAC 360
QY 349 CAACTTAAAGCGAAATTCATAAAGCTGATTCGATGTAGAAATTAGGACATCAGAAAAG 408
Db 361 AAACCTTAAAGGAAATCAACCGGACCGCATCTTAATGCACCAATCTACACGCTCCGATTA 420
QY 409 GAAATTAATAAATAATGATTATATAAATTTGTAGATGCAGGTTATGTATA---TGTAAAGGGA 465
Db 421 AAAGATGATCGGTATCAATATAAATATGTCGCGCGCGGATATGTTTACTACTAGATGGA 480
QY 466 AAAGATGAAATTAAGTGGACTTCAGATTAACAGCAGTTTTCACACCGCTTAGGTTATGAC 525
Db 481 ACAGATGAAATCGAACAGAACTCAGCGCGTAAAGCGGTTACCCACGCTTAGGTTATGAC 540
QY 526 GGTGTTGTATATTTTCGCGAAGACGCTCTCCCATCTTTACCGAGTCGGGAAACGGTG 585
Db 541 GGTGTTGTATATTTTCGCGAAGACGCTCTCTCCCAATCTTACCGAGTCGGGAAACGGTG 600
QY 586 GAATATTTCTGTAACCTGGCAATATATGACCGATGCCCCAACGTCATCGACGAGTAAGGCG 645
Db 601 GAATATTTCTGTAACCTGGCAATATATGACCGATGCCCCAACGTCATCGACGAGTCAGGCG 660
QY 646 GTTGGCAATGCAATTTGGGTTATTAACAATTTATGTTAAACGATGTTGGTCAACTTCT 705
Db 661 GTTGGCAATGCAATTTGGGTTATATACATTTTATGTTAAACGATGTTGGTCAACTTCT 720
QY 706 TATGCGGCTAAGGATGTCGACGAAAGGAAACATCTCTGCTAAATATACGGTAGATTTC 765
Db 721 TATGCGGCTAAGGATGTCGACGAAAGGAAAGAGATCTCTGCCAAATATACGGTTGATT 780
QY 766 GGTAAACAAAACCTGACGCGGAGCTGATTAAAAACCAATATGT-----CAAACCCAGT 819
Db 781 GATAACAAAACCAATGAATGCAAGCTGATTAAAAATCAGTATGCGAAATAAAAAGAT 840
QY 820 GAGAAGCAAAAACCGCTGACCAATTTACATCCTGCGGATTTAAACCGGCAACCGCTTT 879
Db 841 GAAACCAAAAACCGCTGACCAATTTACGACATTTACTGCAAAAATTTGGACGGCAACCGCTTT 900
QY 880 ACCGCGAGTGCCAAGTCAATCTGATTTTAGCGAAAGCCATGCCAATAGGAGCAATTG 939
Db 901 ACCGCGAGTGCCAAGTCAATCTGATTTAGCGAAACCTTTGCCGGTATAGCGCTTTG 960
QY 940 TTTTTCATGCGGATGCCGATCAGCGGCTTAGGGCGGTTTTTTTTCGGCGATAGGGGAA 999
Db 961 TTTTTCATGCGGATGCCGATCAGCGGCTTAGGGCGGTTTTTTTTCGGCGATAGCGAGAA 1020
QY 1000 GAGCTTGGCGGACGGTTTATCAGCAACGACACAGGATTCGCGTGTATTCGAGGCAAA 1059
Db 1021 GAGCTTGGCGGACGGTTTATCAGCAACGACACAGGATTCGCGGCTATTCGAGGCAAA 1080
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Qy 1060 CA-----AAATAGCCCGTGCCTGCTGGAAACACACC 1092
Db AAAACAGAGACAGCAAAACGACAGATACAAAACCTGCCCTGCCGTCTGGAAACACACC 1140
Qy AAAATCTTGGATCTCTGAAATTTCCGTGATGAGGCAAGTGTGAAATTCGCCGACCG 1152
Db AAAATCTTGGATCTCTGAAATTTCCGTGATGAGGCAAGTGTGAAATTCGCCGACCG 1200
Qy TTTGCCATTTCTCCTATGCCCGATTTTGGTCAATCCGACAAATCTTGTTCGAAAGGAT 1212
Db TTTGCCATTTCTCCTATGCCCGATTTTGGTCAATCCGACAAATCTTGTTCGAAAGGAT 1260
Qy GAAATCTTGGTGTAGCCAGAGAAACATCGAGCTTCCGACGCGGAGAAATGACC 1272
Db GAAATCTTGGTGTAGCCAGAGAAACATCGAGCTTCCGACGCGGAGAAATGACC 1320
Qy GTCAGTGTCTTGTGCGACTTTTGAACCTATGAACTCGACGCGATATAAAACCGAACG 1332
Db GTCAGTGTCTTGTGCGACTTTTGAACCTATGAACTCGACGCGATATAAAACCGAACG 1380
Qy CCGCGCCGCAACCCGAGGC-----GCAGGACGAGAGATTCGGAATTCAT 1380
Db CCGCGCAAGTAAACCAAGCGGAGATATAAGGGAGGATGAAGGGTGCAGGGCTTCAT 1440
Qy AATGGCGAAGAAAGCAAGACGAAATCGCGCATGAGAGAGAGCACCAGAGATGCACC 1440
Db AACGACGAAAGCAAGCAAGCGAGCCGTAGAGACGAAAGCGCGCAAGAGAGCAAACT 1500
Qy GCAGGATGAAGGACGAGGAGAGCAAGCAAGCCAC-----AGAAAAAC 1482
Db TCCGAAGAGGATATGCGGAGAGACGAGAGCAACCGCGGAGAGAAACCGAGAAAT 1560
Qy GAAGACGCGGAGAGAGACGAGCTGAAGAACCTGAAGAGAAATCGTCGCGAGAGCGAAC 1542
Db GATGAAGCCGAGAGAGAGAGAGTTGAAGAACCGGAGAAATTCGCCGCGAGAGCGAAC 1620
Qy GCGAGTTCAAGCGCATCTGCTGCTGCGGAGCTCTAAGGCGAGGATATCGACCTT 1602
Db GCGGTTTCAAGCGCATCTGCTGCTGCGGAGCTCTAAGGCGAGGATATCGACCTT 1680
Qy TTCCTGAAAGGTATCCGACGCGCATCGGCAAAACCCATTCAATGGGACAAATCAGGCGAT 1662
Db TTCCTGAAAGGTATCCGACGCGCATCGGCAAAACCCATTCAATGGGACAAATCAGGCGAT 1740
Qy ACCGCACTTGGGAAGCGGTATCGGCAAAACCCATTCAATGGGACAAATCAGGCGAT 1722
Db ACCGCACTTGGGAAGCGGTATCGGCAAAACCCATTCAATGGGACAAATCAGGCGAT 1800
Qy GAGCGGCAAAAGCAGATTTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAAGCTG 1782
Db AAAGCGCAAAAGCAGATTTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAAGCTG 1860
Qy ACGGAGAAACCGGTGTAGAACCTGTTTCCGTTATTTGAAACCGGCTGATTCAGGCGAAC 1842
Db ACGGAGAAACCGGTGTAGAACCTGTTTCCGTTATTTGAAACCGGCTGATTCAGGCGAAC 1920
Qy GGTTCCTATGCGACAGCGGCACTCGGATGACGCGATCGACCTTTCGCGGAGGTTG 1902
Db GGTTCCTATGCGACAGCGGCACTCGGATGACGCGATCGACCTTTCGCGGAGGTTG 1980
Qy ACCAAACCGCAGATTTTCAAGCTATGATCTTCGTGTAGAGGAGGATTTTACGCGCG 1962
Db ACCGACCCCAAAACATTTCAAGCTATGATCTTCGTGTAGAGGAGGATTTTACGCGCG 2040
Qy AAGCGGAGGATTCGCGGATATTTTCAATATGATGGGAAATCTCTTGATATACT 2022
Db AAGCGGAGGATTCGCGGATATTTTCAATATGATGGGAAATCTCTTGATATACT 2100
Qy GAAAGTACTGAAAAATAAGCTGAAGCTGATGTGATGTGATGTGATGTGATGTGAT 2082
Db GAAATATGAAAAATAAGCTGAAGCTGATGTGATGTGATGTGATGTGATGTGAT 2160

Qy 2083 GCTGATCTGATGTTG---AACAGTTAAAC---TGAAGTTAAACCCCAATTCGGCGTG 2136
Db 2161 GTTGAAGCTGATGTTGGCAACAGTTAGAACCTGATGAGTTAAACACAAATTCGGCGTG 2220
Qy 2137 GTATTCGGTCCGAAAGAGATAATAAAGAGGTGAAAAA 2175
Db 2221 GTATTCGGTCCGAAAGAGATAATAAAGAGGTGAAAAA 2259

RESULT 4
US-10-282-122A-29815
; Sequence 29815, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29815
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-282-122A-29815

Query Match 66.9%; Score 1454.8; DB 13; Length 2226;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 1839; Conservative 0; Mismatches 297; Indels 126; Gaps 8;

Qy 1 ATGTCTAAACCGAATATGCGGCAATGTTGTTGGCCCTTACTTTTGGCATCTTGTATC 60
Db 1 ATGTCTAAACCGAATATGCGGCAATGTTGTTGGCCCTTACTTTTGGCATCTTGTATC 60
Qy 61 GCGCGCAATTTTCGGCGTGCAGCTGTTCCGAATCAACGCGACCGTACCCCTACT 120
Db 61 GCGCGCAATTTTCGGCGTGCAGCTGTTGCGAATCAACGCGACCGTACCCCTACT 120
Qy 121 TTCAAGTCTAAGGAGCTTCCCACTCGGCCCTCGCCAAACCTTCTATAGAAATCAGCG 180

Db 121 TTCAAGTCTAAGAGCGTTTCCCACTTTCGCCCCCTGCGGGCCTTCGGTAGAAAACCAACGCCG 180
QY 181 GTCAACGGGCCCGCGTGGTGGGCAATCGCGTGCCTGCAAGGGCGGAATACGTGCTTTTCAT 240
Db 181 GTCAACGGGCCCGCGTGGTGGGCAATCGCGTGCCTGCAAGGGCGGAATACGTGCTTTTCAT 240
QY 241 CGTGAAGATGGCAGCGGAATTCGAATPAGCAAAACAAGCAGAAGAAAGCTGTGCTTTCAA 300
Db 241 CGTGAAGATGGCAGCGGAATTCGCGATAGCAAAACAAGCAGAAGAAAGCTGTGCTTTAAA 300
QY 301 GAAGGTGATGTTCTGTTTTATACGGTTCAABAGGAATAACTTCAACACTTAAAGC 360
Db 301 GAAGGTGATGTTCTGTTTTATACGGTTCCAAAAAGATAAATTCACGAGCTTAAAGAT 360
QY 361 GAAATTCATAAAGCTGATTCGATGTAGAAAATAGGACATCAGAAAAGGAAAAATAAAAA 420
Db 361 AAAATTCATCAACGCAATCTAATGTAGAAAATAGGACATCAGAAAATGAAAATAAAAA 420
QY 421 TATGATTATAAATTTGTAGATGACGGTTATGTATA--TGTAAGGAAAAAGATGAAAT 477
Db 421 TATGGTTATGAATTTGTAGATGACGGTTATGTATACTACAAAGGAAAAAGATGAAAT 480
QY 478 AAGTGCATTCAGATTCAGACAGTTTCCAAACCGCTTAGGTTATGACGGTTTGTATAT 537
Db 481 GAGTGGACTTCAMATCACAAGCAGTTTACCTACCGGTTTGGTTATGACGGTTTGTATAT 540
QY 538 TATTCGGAGAACGTCTCTCCCAATCTTTACCGAGTCCGGGAACGGTGGAAATATCTGGT 597
Db 541 TATTCGGAGAACATCTTTCGCAATCTTTACCGAGCGCGGGAACGGTGGAAATATCTGGC 600
QY 598 AACTGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTAAAGC--GGTTGCAAT 654
Db 601 AACTGCAATATATGACCGATGCCATACGTCATCGAACAGGAAAAAGCAGAGATCCTAGC 660
QY 655 GAACAATTTGGTTATTACACATTTATGTTATGTTAGTGTGTTGGTGCACATCTTATGGGCT 714
Db 661 GAAGATTTGGTTATTATCGTTATTACGGTCAAAATGTGCGAGCAATCTTATGCTGG 720
QY 715 AAGGATGTGACGAAAGGAAAAACATCTCTGTAAATATACGGTAGATTTTCGGTAACAAA 774
Db 721 ACTGCCGACGACGAGAGGAAAAACATCTGCGGATATACGGTAGATTTTCGGTAGAAA 780
QY 775 ACCCTGACGGGAGCTGATTTAAACCAATATGT---CAAAACCGAGTAGAAGCAAAA 831
Db 781 ACTTTGACGGGTAATTAATTAATAATCAGTATGTGCAAAAGAAAAACCGATGAAAGAAA 840
QY 832 CGCTGACCATTTACAACATCACTGCCGATTTAAACGGCAACCGCTTTACCGCAGTGC 891
Db 841 CGCTGACCATTTACACATTTACTGCAATTTGCAACATTTGGCAGGCAACCGCTTTACCGG 900
QY 892 AAGGTCAATCTGATTTAGCGAAAAGCCATGCAATAAGGAGCATTTGTTTTTCCATGCC 951
Db 901 AAAAGTTAACACCGAGGTGAAGACGAAACACGCTGATAAAGCAATTTGTTTTCCATACC 960
QY 952 GATCGGATCAGCGCTTGAGGGCGGTTTTTCGGGATAGGGGGAAGAGCTTGCAGGA 1011
Db 961 GATCGGATCAGCGCTTGAGGGCGGTTTTTCGGGATAGGGGGAAGAGCTTGCAGGA 1020
QY 1012 CGGTTTTATCAGCAACGACAGCGTATTCGGTGTATTTCGAGGCAACAAAATAGCCCC 1071
Db 1021 CGGTTTTATCAGCAACGAGCGTATTCGGGCTATTTCGAGGCAACAAAATAGCCCC 1080
QY 1072 G-----TGCGTCTGGAACACACCAAAATCTTG 1101
Db 1081 GCATCAAGCGCATCAGATCAAAATCTGCTATGCGCTGTGAAAAACACCAAAATCTTG 1140
QY 1102 GATTTCTGAAATTTCCGTTGATGAGCAAGTGTGAAATCCCGACCGTTGGCAT 1161
Db 1141 GATTTCTGAAATTTCCGTTGACAGGCGACTGATAGCAATGCCCGTAAAGTTTGCAT 1200
QY 1162 TCTCCTATCCCGAATTTTGGTTCATCCGACAACTTCTTGTGCAAGGCGATGAAATTCCT 1221
Db 1201 TCCCTATGCCGATTTTGGTTCATCCGACAACTTCTTGTGCAAGGCGGTGAAATCTCC 1260

RESULT 5

US-10-735-098-3

; Sequence 3, Application US/10735098

QY 1222 TTGTTAGCCAGAGAAAAACCATCGAGCTTCCGACGCGAGGAAAAATGACCGTCAAGTCT 1281
Db 1261 TTGCTCAAGATACTCAACCATCGATCTTCCGACGCGCAGGAAAAATGACCGTCAAGTCT 1320
QY 1282 TGTTCGACATTTTTCGCTTATGTGAAACTTCGACGCGATAAAAACCGAACCCCGCGCGCC 1341
Db 1321 TGTTCGACATTTTTCGCTTATGTGAAACTTCGACGCGATAAAAACCGAACCCCGCGCGCAAGT 1380
QY 1342 AAACCGAACGCGCAGACGAGAGA--GGATTCCGACATTTGATATATGGCAGAAAGCGGAA 1398
Db 1381 AAACCGAACGCGCAGACGAGAGATTCGAAAGTGAATTTGGTGAAGACCGAGGAAAAATGAA 1440
QY 1399 GACCAATTCGCGATCAAGAAGAAAGCACCGAAGATGACGCGCAGGAGATGAAGCAGC 1458
Db 1441 GAGGATTTGGTCTGCTGAGAGAGAAACACGGAAGACGAGTCTGTAGAAGATGAAGACGA 1500
QY 1459 GAAGAAGACGAAGCCACAGAAAAC----- 1482
Db 1501 GAAGAAGACGAAGTTCGGAAGATGCTAAACAGTGAAGACGAAGAAATCGCCGAAGAA 1560
QY 1483 -----GAAGACGGCGAAGACGAGCTGAAGAACCTGAAGAAATTCGTCGGCAGAA 1536
Db 1561 GATGATGATGAAGCCGAAGAGGAGGAAGTTGAAGAACCCGGAAGAAATTCGCCGAGAA 1620
QY 1537 GGCAAC---GGCAGTTTCAAAACGCCATCTCTGCTCTCCCGAAGCCCTCTAAAGCAGCGAT 1593
Db 1621 GCGCGCGGTGGCGTTTACGCGCATCCCGCGCTTCGAGACCCCTTAAGGACAGGAC 1680
QY 1594 ATCGACCTTTTCTGAAAGGTATCCGACGCGCAAAACGAATATTCGCAAACTGGAGAA 1653
Db 1681 ATCGACCTTTTCTGAAAGGTATCCGACGCGGGAAGCGACATTCGCAAACTGGAGAA 1740
QY 1654 GCACGCTATACCGGCACCTTTGGGAAGCGGTATCGGCAAAACCCATTCATGGGACAATCAT 1713
Db 1741 GCACGCTATACCGGCACCTTTGGGAAGCGGTATCAGCAAAACCCATTCATGGGTAATAAG 1800
QY 1714 GCGGATAAAGAAAGCGGCAAAAGCAGTATTTACCGTTGATTTTCGGCAAGAAATCGATTTCC 1773
Db 1801 GCGGATAAAGAAAGCGGCAAAAGCAGATTTTGAAGTTGATTTTCGGCAAGAAATCGATTTCC 1860
QY 1774 GGAAGCTGACGAGGAAAAACCGTGTAGAACCTGCTTTCCGTTATTTGAAAACCGCGTGAT 1833
Db 1861 GGAAGCTGACGAGGAAAAACCGTGTAGAACCTGCTTTCTATATTTGAAAAGGTGAT 1920
QY 1834 GAGGCAAGCGTTTCCATGCGACGCGCACCTCGGATGACGCGATCGACCTTTCCGGG 1893
Db 1921 GATGGCAACGGTTTCCACGCGACGACGCACTCGGATACCGGCACTCAATCTTTCCGGA 1980
QY 1894 CAGGGTTTCGACCAAAACCGCAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGAGATTT 1953
Db 1981 AATGGTTTCGACCAACCCCAAAACCTTCCAAAGCTAGTATCTTCGTGTAGAGGAGATTT 2040
QY 1954 TACGGCCGAGGCGGAGGAAATTCGGCGGTATTTTCAATAATGATGGGAAAAATCTCT 2013
Db 2041 TACGGCCGAGGCGGAGGAAATTCGGCGGTATTTTCAATAAGGATGGGAAAAATCTCT 2100
QY 2014 GGTATAACTGAAGTACTGAAATAAAGTTGAAGCTGATTTGATGTTGATGTTGAT 2073
Db 2101 GATATAACTGAAGATATTGACAAATGAAATTTGAAGCTGA----- 2138
QY 2074 GATGTTGATGCTGATGCTGATTTGAAACAGTTTAAACCTTGAAGTTAAACCCCAATTCGGC 2133
Db 2139 -----TGTCGCGCAACAGTTTAGAACCTGAGTTAAACCCCAATTCGGC 2181
QY 2134 GTGCTATTTCGGTGCAGAGAAAGATATAAGAGGTGGAAAAA 2175
Db 2182 GTGCTATTTCGGTGCAGAGAAAGATATGAGGAGGTGGAAAAA 2223

```

; Publication No.: US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M981
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2166)
; US-10-735-098-3

Query Match          60.0%; Score 1304.8; DB 17; Length 2169;
Best Local Similarity 79.1%; Pred. No. 9e-300;
Matches 1675; Conservative 0; Mismatches 332; Indels 111; Gaps 6;

QY 1 ATGTGTAACCGAATTATGGCGGCAATGTCCTGTGTGCGCCCTACTTTTGGGCATCTGTATC 60
DB 1 ATGTGTAACCGAATTATGGCGGCAATGTCCTGTGTGCGCCCTACTTTTGGGCATCTGTATC 60

QY 61 GGCGCAATTTCCGGGTGCAGCTGTGTGCAATCAACGCGCGACGCGGTACCCCGTCAC 120
QY 61 GGCGCAATTTCCGGGTGCAGCTGTGTGCAATCAACGCGCGACGCGGTACCCCGTCAC 120

QY 121 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTCCGCAAACTTCTTAGAAATCACGCCG 180
DB 121 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTCCGCAAACTTCTTAGAAATCACGCCG 180

QY 181 GTCAACCGCGCCCGTGGTGGCGCAATGGCGTGCAGCGCGCAATCTGCTTTTCAT 240
DB 181 GTCAACCGCGCCCGTGGTGGCGCAATGGCGTGCAGCGCGCAATCTGCTTTTCAT 240

QY 181 GTCAACCGCGCCCGTGGTGGCGCAATGGCGTGCAGCGCGCAATCTGCTTTTCAT 240
DB 181 GTCAACCGCGCCCGTGGTGGCGCAATGGCGTGCAGCGCGCAATCTGCTTTTCAT 240

QY 241 CGTGAAGATGGCACCGGAATTCGAATAGCAAAACGAGCAGAGAAAGAGCTGCTCGTTCAA 300
DB 241 CGTGAAGATGGCACCGGAATTCGAATAGCAAAACGAGCAGAGAAAGAGCTGCTCGTTCAA 300

QY 301 GAAAGTGATGTTCTGCTTTTATACCGTTTCAAAAGGAAATAAACTTCAACAACCTTAAAGC 360
DB 301 GAAAGTGATGTTCTGCTTTTATACCGTTTCAAAAGGAAATAAACTTCAACAACCTTAAAGC 360

QY 361 GAAATTCATAACGCTGATTCGATAGAAATTAGACATCAGAAAGGAAATAAABAAA 420
DB 361 GAAATTCATAACGCTGATTCGATAGAAATTAGACATCAGAAAGGAAATAAABAAA 420

QY 421 TATGATTATAAATTTAGATCCAGTTATGAT -- -ATGTAAAGGAAAGATGAAAT 477
DB 421 TATGATTATAAATTTAGATCCAGTTATGAT -- -ATGTAAAGGAAAGATGAAAT 477

QY 478 AAGTGACATTCAGATTACAGCAGTTTCCACCGCTTAGGTTATGACGGTTTGTATAT 537
DB 478 AAGTGACATTCAGATTACAGCAGTTTCCACCGCTTAGGTTATGACGGTTTGTATAT 537

QY 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTAGGCTATGACGGTTTGTATAT 540
DB 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTAGGCTATGACGGTTTGTATAT 540

QY 538 TATTCGGGAGAACGTCCTTCCCAATCTTTACGAGTGGGGAACGGTGAATATTTCTGTT 597
DB 538 TATTCGGGAGAACGTCCTTCCCAATCTTTACGAGTGGGGAACGGTGAATATTTCTGTT 597

QY 541 TATCTCGGAGAACATCTCTCCCAATCTTTACCGAGCGGGGAACGGTGAATATTTCCGCG 600
DB 541 TATCTCGGAGAACATCTCTCCCAATCTTTACCGAGCGGGGAACGGTGAATATTTCCGCG 600

QY 598 AACTGGCAATATATGACCGATGCCAACTCANTCGAGCGGTAAAGCGGTTGGCATTGAC 657
DB 598 AACTGGCAATATATGACCGATGCCAACTCANTCGAGCGGTAAAGCGGTTGGCATTGAC 657

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Qy	1663	ACCGGC	ACTTGGG	AGCGGTATCGG	CAAA	CCCATTTCAATGGG	ACAATCATGCGGAT	---	1719
Db	1741	ACCGGC	ACTTGGG	AAGCGGTATCGG	CGTATCGG	CGATAGAG	AGCGCAACGCTAGATGGC		1800
Qy	1720	-----	AAAGA	AGCGGCAAAAG	CAGGTATT	TACCGTT			1749
Db	1801	ACTACG	TCCATTCAA	AAAGTAGTATG	CGAATCAAGCGG	CAAAAGCAGAA	TTTGACGTT		1860
Qy	1750	GATTT	CGGCAAGAAATCGAT	TTCCGGAACGCTGAC	GGAGAAAACGGTGTAG	AAACCTGCT			1809
Db	1861	GATTT	TGGTGGCAAGTTCG	TTTCAGGTAGTGTGAC	AAAAAAATGATACAC	ACCCCGCT			1920
Qy	1810	TTCCGT	TATGAAAACGGCGT	CAATTGAGGCAAA	CGGTTTCCATCGCAG	CGGCGCACTCGG			1869
Db	1921	TTTTAT	TATGAAAAGGTGTGAT	TGATGGCAACGGTTT	CCACGCTTTGGCGG	TACTCGT			1980
Qy	1870	GATCAG	CGCATCGAC	CTTTCGGG	CGAGGTTCGACCAAA	CCGAGATCTTCAAAGCTAAT			1929
Db	1981	GAAAT	CGTGTGATTTGTCTGGG	CAAGTTCGACTAAT	CCCCAAAGTTTAAAG	CCCACT			2040
Qy	1930	GATCTT	CGTGTAGAAGGAGGATTT	TACGGCCCGAAAGCGGAGGAAT	TGGCGGCTATTATT				1989
Db	2041	AACTCT	CTCGTAGAAGAGGATTT	TATGTCCGACAGCGG	CAGAGTTGGGTGGTAA	TATT			2100
Qy	1990	TTCAAT	TAATGATCGGAAA		2007				
Db	2101	ATCGAC	AGTGACCGGAAA		2118				

RESULT 6

RECEIVED
US-10-735-098-9

03-10-733-038-9 : Sequence 9. Application IRS/10725089

; Publication No. US20040731634A1

; GENERAL INFORMATION:

APPLICANT: Pettersson-Fernholm Annika Magnusdotter

APPLICANT: Tommassen, Johannes Petrus Marij
; APPLICANT: Tommassen, Johannes Petrus Marij

TITLE OF INVENTION: Neisseria lactoferrin Binding Protein

; FILE REFERENCE: B45106C1

; CURRENT APPLICATION NUMBER: US/10/735,098

; CURRENT FILING DATE: 2003-12-12

; PRIOR APPLICATION NUMBER: 09/485,760

; PRIOR FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: PCT/EP98/051117

; PRIOR FILING DATE: 1998-08-10

; PRIOR APPLICATION NUMBER: GB

; PRIOR FILING DATE: 1997-08-15

;; PRIOR APPLICATION NUMBER: GB 9805544.8
: PRIOR FILING DATE: 1998-08-05

; PRIOR FILING DATE: 1998-02-05
: NUMBER OF SEQ ID NOS: 12

NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows

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; SOFTWARE: FAS
; SEO ID NO 9

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;   REQ ID NO 3
;   LENGTH: 2124

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TYPE: DNA

ORGANISM: *Neisseria meningitidis* strain 991507

FEATURE:

; NAME/KEY: CDS

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; LOCATION: (1) ... (2121)

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US-10-735-098-9

Query Match

Query Match	59.6%	Score 1296.2;	DB 17;	Length 2124;
Best Local Similarity	79.0%	Score 1296.2;	DB 17;	Length 2124;

2000 local similarity 79.0%; pred. No. 9.9e-298;
Matches 1672: Conservative 0. Micromatch 200

Accession	Size	Conservative	0	Mismatches	373	Indels	72	Gaps
1	ATGTGTAACCGAATTATGGCGCAATGCTCTTGGCCCTTACTTTTGGCATCTCTGTATC	60						
Db	1	ATGTGTAACCGAATTATGGCGCAATGCTCTTGGCCCTTACTTTTGGCATCTCTGTATC	60					
2	GGCGGCAATTTCGGCGGTGCAGCCTGTTTGTGCAATCAACGGCGACCGGTACCCCGTCACT	120						
Db	61	GGCGGCAATTTCGGCGGTGCAGCCTGTTTGTGCAATCAACGGCGACCGGTACCCCGTCACT	120					
3	TTCAAGCTCAAGGACGTTCCCATCTCGCCGCCCTTGCCCAACCTTCTATAGAAATCAACGGC	180						

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Db 1201 TCCACTATGCCCGATTCTTGTCATCCCGACAACTTCTTGTGGAAGGCGTGAATTCCT 1260
Qy 1222 TTGTTAGCCGAAGAAACCATCGAGCTTCCGACGGCAGAAATGACCGTCAGTGCT 1281
Db 1261 TTGTTAAACAAAGAACCAACCATCGATCTTCCGACGGCAGAAATGACCGTCGCTGCT 1320
Qy 1282 TGTTCGCACTTTTGAACCTATGTGAACCTCGGACGATATAAAACCGAACGCGCCGCGCC 1341
Db 1321 TGTTCGCACTTTTGAACCTATGTGAACCTCGGACGATATAAAACCGAACGCGCCGCGCT 1380
Qy 1342 AAACCGAAGGCGCA-----GGACGAAGAGGATTCGGACATTTGATTAATGGCGAA 1389
Db 1381 CAACCGAAGGCGCAGGATGAAGAGGGGACGACGAGAGGCTGTAGCGCTTGTATAACCGTAAA 1440
Qy 1390 GAAAGCGAAGCGAAATCGGCGATGAAGAGAGGACCGACCAAGATGACGCGCGAGAT 1449
Db 1441 GAAAGCGAAGCGAAATCGGCGATGAAGAGAGGACCGACCAAGATGCTGTAGAGATGAA 1500
Qy 1450 GAAAGCGAAGCGAAGAGCGACGACGAAACCGAAGACGCGGAGAGACGACGCTGAA 1509
Db 1501 GACGAAGATGAAGACGAGAGAGAAATCGAAGAGAACCTGAAGAGAGCTGAAGAGAA 1560
Qy 1510 GAACTCTGAAGAGAAATCGTCGCGC---AGAAGCGCAACGCGAGTTCAAACGCCATCTGCT 1566
Db 1561 GAAACCGAAGAGAAATTCGCGCGCAGAGAGAGCAAGCGCGGTTTCAGGCGAGCATCTGCGCC 1620
Qy 1567 GTCGCGGAGGCTCTAAAGGCGAGGATATCGACCTTTTCCTGAAAGGTATCGGACGGCA 1626
Db 1621 ACTCGGAGGCTCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATTCGCGACGCG 1680
Qy 1627 GAAACGAATATTCGCGAACTGGAGAGACGCTATACCGGCACCTTGGGAGCGCGTATC 1686
Db 1681 GAACCGGACATTCGAAAGAACGAGACGCGCGGATATACCGGCACTTGGGAGCGCGTATC 1740
Qy 1687 GGC-----AAACCCATTCAATGGGACAAATCATCGGATATAAGAGAGCGCA 1731
Db 1741 GCGGTATCGGATAGTGGTACGTCCTCAATCAAAAGGATAGCTATGCG---AATCAAGGGGCA 1797
Qy 1732 AAACGAGTATTTACGTTGATTTTCGGCAAGAAATCGATTTTCGGACGCTGACGAGGAA 1791
Db 1798 AAAGCAGAAATTTACCGTTGATTTTGAACGCAAGACGGTGTCCGGATCTGACAGAAAA 1857
Qy 1792 AACGCTGAGAACCTGCTTTCCGTATTGAAAGCGCGTGATTGAGGGCAACGGTTTCAT 1851
Db 1858 AATGATACAAACCCCGCTTTTATTTGAAAGAGTGATGACGGTAAACGGTTTCAC 1917
Qy 1852 CGCAGCGCGCACTCGGATGACGGCATCGACCTTTCCGGCGAGGTTGACACCAACCG 1911
Db 1918 GCTTTGGCGCATACTCGGGAGAAACGGTATTGACCTTTCTGGCGAGGTTTCGACTAACCCG 1977
Qy 1912 CAGATCTCAAGCTAATGATCTTCGTGAGAGGAGATTTTACGGCCCGAGCGGAG 1971
Db 1978 AAGAACTTCAAGCGGCAATCTTCTTGTAAACGGCGCTTTTATGGCCCGAGCGGCA 2037
Qy 1972 GAATTTGGCGGTATTATTTTCAATAATGATGGAAATCTCTTTGATATAACTGAAGGTACT 2031
Db 2038 GAATTTGGCGGTATTATTTATTCAGACGACCGGAAATTCGGTTCGGGTATTTTGGGCGGAA 2097
Qy 2032 GAAATAAAGTTGAAGC 2048
Db 2098 AAAGATGACAAGGAGC 2114
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RESULT 7

US-10-343-561-15

; Sequence 15, Application US/10343561

; Publication No. US20040126389A1

; GENERAL INFORMATION:

; APPLICANT: Berthet, Francois-Xavier Jacques

; APPLICANT: Dalemans, Wilfried

; APPLICANT: Denoel, Philippe

; APPLICANT: Dequesne, Guy

; APPLICANT: Feron, Christiane

```
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thiry, Georges
; APPLICANT: Thonnard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; TITLE OF INVENTION: Vesicles from Gram Negative Bacteria
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343,561
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15
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Query Match 31.2%; Score 678.6; DB 17; Length 1000;

Best Local Similarity 82.4%; Pred. No. 6.3e-151; Indels 13; Gaps 4;

Matches 830; Conservative 0; Mismatches 164;

Qy 1174 GATTTTGTCTATCCCGACAACTTCTTGTGCAAGGGCATGAAATTCCTTTGTTAGCCAA 1233

Db 1 GATTTTGTCTATCCCGACAACTTCTTGTGCAAGGGCATGAAATTCCTTTGTTAGCCAA 60

Qy 1234 GAGAAACCATCGAGCTTCCGACGGCAGGAAATGACCGTCAGTCTTGTTCGACTTT 1293

Db 61 GAGAAACCATCGAGCTTCCGATGGCAGGAAATGACCGTCGCTGCTTGTTCGACTTT 120

Qy 1294 TTGACCTATGTGAAACTCGGACGATATAAAACCGAACCCCGCGCCAAACCGAAGCG 1353

Db 121 TTGACCTATGTGAAACTCGGACGATATAAAACCGAACCCCGCGCAAGTAAACCAAGCG 180

Qy 1354 CAGGACGAA---GAGGATTCGGACATTTGATATGCGGAGAAAGCGAAGCAATCGC 1410

Db 181 GAAGATAAAGGGAGGATGAAGAGATGTCAGCGCTTGTTAACTCGAAGAAAGCGAAGCG 240

Qy 1411 GATGAGAGAGAGGACCGAAGATGACCGCCGACGAGATGAGCGCAGGAGAGAGACGAA 1470

Db 241 GAACTTTCCGAAGATGAAGCGGAGAGACCGAAGAAATCGTCGAAGAAAGACCCGAGAA 300

Qy 1471 GCCACAGAAACGAAAGCGGAGAGAGACGAAAGCTGAAGAACCTGAAGAAAGATCGTCG 1530

Db 301 GAAGCTGAGAGAGAGAGAGCTGAACCCAAAGAGTTGAGAAACCGAAGAAATCGCG 360

Qy 1531 GCAGAAGCAACGGCA---GTTCAACGCCATCTCTGCTGTCGCGAAGACCTCTAAAGCG 1587

Db 361 ACAGAAGAAAGCGCAGCGTTCAACGCCATCTCTGCTGCTCGAAGACCTCTAAAGCG 420

Qy 1588 AGGATATCGACCTTTTCTGAAAGGATTCGCGACGCGAGAAACGAAATATTTCCGCAACT 1647

Db 421 AGGACATCGACCTTTTCTGAAAGGATTCGCGACGCGGAGCGGACATTTCCAGAAACC 480

Qy 1648 GGAGAGCACCTATACCGCATTGGGAGCGGTATCGGCAACCCATTCATATGGGAC 1707

Db 481 GGAAAGCACACTATACCGCATTGGGAGCGGTATCGGCAACCCATTCATATGGGAC 540

Qy 1708 AATCATCGGATAAAGAGAGCGGCAAAACAGCAGTATTTACCGTTGATTTTCGGCAAGAAATCG 1767

Db 541 AATCAGCGCGATAAAGAGCGGCAAAACAGCAGTATTTACCGTTAAATTCGCGGAGAAATCG 600

Qy 1768 ATTTCCGGAACGCTGACGCGAGAAACCGGTGTAGAACCTGCTTCCGTTATTCGAACCGC 1827

Db 601 ATTTCCGGAACGCTGACGCGAGAAACCGGTGTAGAACCTGCTTCCGTTATTCGAACCGC 660

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QY 1828 GTGATTGAGGGCAACGGTTTCATGCGACAGCGCGCACTCGGGATGACGGCATCGACCTT 1887
Db 661 AAGATTGAGGGCAACGGTTTCATGCGCAACAGCAGCAGCTCGTGAGAACGGCATCAATCTT 720
QY 1888 TCGGGCAGGGTTCGACCAACCGCAGATCTTCAAGCTTAATGATCTTCTGTAGAGGA 1947
Db 721 TCGGGAATGGTTTCGACCAACCCAGAACCTTCCAAGCTAGTGATCTTCTGTAGAGGA 780
QY 1948 GGATTTTACGGCCGAGGCGGAGGAATTGGCGGTATTATTTTCAATAATGATGGAAA 2007
Db 781 GGATTTTACGGCCGCGA-CGGGAGGAATTGGCGGTATTATTTTCAATAAGGATGGAAA 839
QY 2008 TCTCTTGGTATACTGAAGTACTGAAATAAAGTTGAAGCTGATGTTGATGTTGATGTT 2067
Db 840 TCTCTTGGTATACTGAAGTACTGAAATAAAGTTGAAGCTGATGTTGATGTTGATGTT 899
QY 2068 GATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 2127
Db 900 GAAGCTGAACCTGGTGTTCGAAACAGTTAGAAC-----CTGATGAAGTTAAACCCCAA 953
QY 2128 TTCGGCGTGTATTTCGGTTCGGAAGAAAGATAATAAAGAGTGGAAA 2174
Db 954 TTCGGCGTGTATTTCGGTTCGGAAGAAAGATAATAAAGAGTGGAAA 1000

RESULT 8
US-10-467-534-80
; Sequence 80, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verilant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-80

Query Match 8.0%; Score 174.2; DB 17; Length 3300;
Best Local Similarity 77.2%; Pred. No. 1.4e-30;
Matches 240; Conservative 0; Mismatches 38; Indels 33; Gaps 1;

QY 1865 CTCGGGATGACGGCATCGACCTTTCGGCGAGGTTTCGACCAACCGCATCTTCAAG 1924
Db 1 CTCGGGATGACGGCATCAATCTTTCGGGAAATGGTTGCACTAATCTCTCAAGTTTCAAAG 60
QY 1925 TTAATGATCTTCTGTAGAGGAGGATTTTACGGCCGAGGAGGATTTGGCGGTA 1984
Db 61 CGGCAATCTTCTGTAGCGGCGCTTTTACGGCCGAGGAGGATTTGGCGGTA 120
QY 1985 TTAATTTCAATGATGGGAATCTCTTGGTATTAATCTGAAGTACTGAAAATAAAGTTG 2044
Db 121 TTAATTTCAATGATGGGAATCTCTTGGTATTAATCTGAAGTACTGAAAATAAAGTTG 180
QY 2045 AAGCTGATCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2104
Db 181 AATGAACTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 207
QY 2105 TAAACCTGAGTTAAACCCCAATTCGGCGTGTATTTCGGTTCGGAAGAAAGATAATAAG 2164
Db 208 TAGAACCTGAGTTAAACCCCAATTCGGCGTGTATTTCGGTTCGGAAGAAAGATAATAAG 267
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QY 2165 AGGTGAAAAA 2175
Db 268 AGGTGAAAAA 278
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RESULT 9

US-10-087-192-463/c

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; Sequence 463, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 31124
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31124)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-463
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Query Match 3.8%; Score 81.6; DB 13; Length 31124;

Best Local Similarity 61.1%; Pred. No. 5.8e-08; Matches 132; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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QY 1322 AAACCGAACGCGCCGCCAAACCGAAGCGCGACGAGGAGGATTCGGACATTGATA 1381
Db 18612 AAAAGAAAAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 18553
QY 1382 ATGGCGAAGAAAGCGAAGACGAAATTCGGCGATGAGAAGACCGACCGAGATGCGCGG 1441
Db 18552 AAGAAGAGAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 18493
QY 1442 CAGGAGATGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501
Db 18492 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 18433
QY 1502 AAGCTGAAGAACCTGAAGAAGAAATCGTCGCGCAGAAG 1537
Db 18432 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 18397
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RESULT 10

US-10-087-192-1627/c

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; Sequence 1627, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
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US-10-027-632-269927/c
; Sequence 269927, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269927
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-269927

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Best Local Similarity 63.0%; Pred. No. 3.9e-08;
Matches 119; Conservative 1; Mismatches 69; Indels 0; Gaps 0;

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Db 452 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393
QY 1409 GCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1468
Db 392 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 333
QY 1469 AAGCCACAGAAACGGAAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1528
Db 332 AAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 273
QY 1529 CGGAGAG 1537
Db 272 AAGAAGAG 264

RESULT 14
US-09-864-761-19262/c
; Sequence 19262, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19262
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011416.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 35
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: P05156, EVALUE 9.40e+00
; OTHER INFORMATION: NT HIT: U67539.1, EVALUE 7.40e-01
; OTHER INFORMATION: EST_HUMAN HIT: BF129635.1, EVALUE 1.10e+00
US-09-864-761-19262

Query Match          3.6%; Score 78; DB 9; Length 305;
Best Local Similarity 63.2%; Pred. No. 2.8e-08;
Matches 120; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1347 GAAGGCGAGGAGGAGGATTCGACATTGATATCGGAGGAGGAGGAGGAGGAGG 1406
Db 202 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 143
QY 1407 CGGCGATGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1466
Db 142 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 83
QY 1467 CGAAGCCACAGAAACGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1526
Db 82 AGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 23
QY 1527 GTCGGCAGAA 1536
Db 22 ATTAAAGAA 13
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 19:47:16 ; Search time 782 Seconds

(without alignments)

8819.139 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5669501 seqs, 1585417693 residues

Total number of hits satisfying chosen parameters: 11339002

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
- 9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	80	3.7	601	5	US-09-949-003C-61279
2	79.6	3.7	40778	5	US-09-949-003C-4003
3	79.6	3.7	40779	5	US-09-949-003C-5256
4	79	3.6	379	1	PCT-US02-39555A-2260
5	77.4	3.6	336	7	US-10-674-124A-14888
6	76.4	3.5	472	7	US-10-674-124A-5858
7	76.4	3.5	104595	7	US-10-796-307-8719
8	75.8	3.5	105046	5	US-09-949-003C-4057
9	75.8	3.5	105046	6	US-10-896-891-562
10	75.4	3.5	450000	7	US-10-650-449A-3
11	74.2	3.4	6074	6	US-10-868-184A-12927
12	74.2	3.4	6074	8	US-10-868-184A-12927
13	74.2	3.4	6074	8	US-10-868-184A-12927
14	73.4	3.4	186191	1	PCT-US04-02652-10794
15	73.4	3.4	186191	7	US-10-767-471-10794
16	72.2	3.3	195909	5	US-09-949-003C-3723
17	72.2	3.3	195910	5	US-09-949-003C-5418
18	72	3.3	392	7	US-10-674-124A-155
19	71.6	3.3	447	7	US-10-674-124A-6601
20	71.6	3.3	573	7	US-10-674-124A-20334
21	71.6	3.3	678	1	PCT-US04-12047-412
22	71.4	3.3	8917	5	US-09-404-520B-2417
23	71.4	3.3	1091282	6	US-10-915-727-12218
24	71	3.3	840	1	PCT-US04-12047-111

25	71	3.3	2232	7	US-10-808-727-45	Sequence 45, Appl
c 26	71	3.3	263852	7	US-10-812-232-6	Sequence 6, Appli
c 27	71	3.3	816609	9	US-60-550-051-2987	Sequence 2987, Ap
28	70.6	3.2	213541	9	US-60-592-408-149	Sequence 149, App
c 29	70.2	3.2	28037	7	US-10-796-307-8704	Sequence 8704, Ap
30	69.4	3.2	17088	1	PCT-US04-02652-10707	Sequence 10707, A
c 31	69.4	3.2	17088	7	US-10-767-471-10707	Sequence 10707, A
c 32	69.4	3.2	34403	1	PCT-US04-02652-10620	Sequence 10620, A
c 33	69.4	3.2	34403	7	US-10-767-471-10620	Sequence 10620, A
c 34	69.2	3.2	41386	9	US-60-582-609-19329	Sequence 19329, A
c 35	69	3.2	27950	9	US-60-582-609-19329	Sequence 19329, A
36	68.6	3.2	549	1	PCT-US04-11912-5	Sequence 5, Appli
37	68.6	3.2	549	1	PCT-US04-12049-5	Sequence 12217, A
c 38	68.6	3.2	510510	7	US-10-796-280-12217	Sequence 5616, Ap
c 39	68.6	3.2	510510	9	US-60-548-091-5616	Sequence 23154, A
c 40	68.4	3.1	386	7	US-10-674-124A-23154	Sequence 437, App
c 41	68.4	3.1	173354	9	US-60-592-408-437	Sequence 5330, Ap
c 42	68.2	3.1	268	7	US-10-674-124A-5330	Sequence 5649, Ap
43	68	3.1	457	7	US-10-674-124A-5649	Sequence 568, App
c 44	67.6	3.1	148834	9	US-60-592-408-568	Sequence 363, App
45	67.4	3.1	1437	1	PCT-US04-12047-363	

ALIGNMENTS

RESULT 1
US-09-949-003C-61279
; Sequence 61279, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
; DISORDERS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000791
; CURRENT APPLICATION NUMBER: US/09/949,003C
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,446
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 74065
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 61279
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-003C-61279

Query Match 3.7%; Score 80; DB 5; Length 601;
Best Local Similarity 62.9%; Pred. No. 7.5e-10;
Matches 122; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY	1348	AAGCGCAGGACGAGAGGATTCGACATTGATGCGGAGAGGACGACGAAATC	1407
DB	112	AAAGAAGAGGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAA	171
QY	1408	GCGCATGAAGAAGAGGCGCAGATCGACCGCAGGAGATGAAAGCGCGGAGAGAC	1467
DB	172	GAAGAAGAA	231
QY	1468	GAAGCCACAGAAAACGAGACGCGGAGAGACGAGAGGAGAGAGAGAGAGAGAG	1527
DB	232	GAAGAAGAA	291
QY	1528	TCGCGCAGAGGCGAA	1541
DB	292	GAAGAAGAGAGAGAA	305

RESULT 2
US-09-949-003C-4003/c
; Sequence 4003, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC


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Db 2708 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 2649
Qy 1462 GAAGACGAGCCACAGAAAACGAGACGGCGAAGAAGACGAGCTGAGAACCTGAGAA 1521
Db 2648 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 2589
Qy 1522 GAATCGT 1528
Db 2588 AAATCCT 2582

RESULT 14
PCT-US04-02652-10794/c
; Sequence 10794, Application PC/TUS0402652
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: PCT/US04/02652
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10794
; LENGTH: 186191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(186191)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
PCT-US04-02652-10794

Query Match 3.4%; Score 73.4; DB 1; Length 186191;
Best Local Similarity 59.5%; Pred. No. 4.7e-07;
Matches 116; Conservative 4; Mismatches 75; Indels 0; Gaps 0;

Qy 1355 AGGACGAGAGGATTCGGACATTGATTAATGGCGAAGAAGAAAGCGAAGACGAAATCGGCGATG 1414
Db 52398 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 52339
Qy 1415 AAGAAGAAGCCAGCGGCGAAGACGAGATGAAGCGGCGAAGACCTGAAGAAGAAATCGTCGGCAG 1474
Db 52338 GAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 52279
Qy 1475 CAGAAAACGAGACGGCGAAGACGAGACGAGCTGAAGACCTGAAGAAGAAATCGTCGGCAG 1534
Db 52278 AAGAAGAAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 52219
Qy 1535 AAGGCAACGGCAGTT 1549
Db 52218 GAGCGAGGGAGGAT 52204

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Job time : 788 secs
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-767-471-10794

Query Match 3.4%; Score 73.4; DB 7; Length 186191;
Best Local Similarity 59.5%; Pred. No. 4.7e-07;
Matches 116; Conservative 4; Mismatches 75; Indels 0; Gaps 0;

Qy 1355 AGGACGAGAGGATTCGGACATTGATTAATGGCGAAGAAGAAAGCGAAGACGAAATCGGCGATG 1414
Db 52398 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 52339
Qy 1415 AAGAAGAAGCCAGCGGCGAAGACGAGATGAAGCGGCGAAGACCTGAAGAAGAAATCGTCGGCAG 1474
Db 52338 GAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 52279
Qy 1475 CAGAAAACGAGACGGCGAAGACGAGACGAGCTGAAGACCTGAAGAAGAAATCGTCGGCAG 1534
Db 52278 AAGAAGAAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 52219
Qy 1535 AAGGCAACGGCAGTT 1549
Db 52218 GAGCGAGGGAGGAT 52204

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OM nucleic - nucleic search, using sw model

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

BST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gsl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	83.8	3.9	289	14	CAY16220 wdk3c.pk0
C 2	82.8	3.8	754	12	BI454583
C 3	82.2	3.8	739	28	BZ220379
C 4	82	3.8	675	28	BZ104011

5	81.6	3.8	531	14	CD915362
6	81.6	3.8	744	28	BH065422
C 7	81.4	3.7	355	29	CE349803
C 8	81.4	3.7	434	14	CAY45444
C 9	81.2	3.7	265	14	CA607797
C 10	81.2	3.7	719	28	BH360392
C 11	81	3.7	263	13	BU005139
C 12	80.8	3.7	729	29	CE180020
C 13	80.6	3.7	264	13	BQ241566
C 14	80.6	3.7	501	12	BI504790
C 15	80.6	3.7	527	28	AZ279446
C 16	80.4	3.7	960	28	CC143364
C 17	80.2	3.7	799	28	BZ201507
C 18	80.2	3.7	880	28	CE180020
C 19	80.2	3.7	1096	14	AZ529191
C 20	79.6	3.7	341	29	CE510654
C 21	79.6	3.7	551	12	BM650535
C 22	79.4	3.7	540	28	AZ813205
C 23	79.4	3.7	665	13	BU432980
C 24	79.2	3.6	477	14	CD311846
C 25	79.2	3.6	575	10	BF707975
C 26	79	3.6	205	13	BQ241058
C 27	79	3.6	232	29	CG321416
C 28	79	3.6	301	29	CE339332
C 29	79	3.6	546	28	AZ600777
C 30	79	3.6	596	29	CC660549
C 31	79	3.6	558	28	BH346798
C 32	78.6	3.6	421	28	AZ113646
C 33	78.6	3.6	816	28	AZ535744
C 34	78.6	3.6	891	28	AZ683582
C 35	78.6	3.6	924	13	BQ925195
C 36	78.4	3.6	395	29	CE760553
C 37	78.2	3.6	605	28	BZ222147
C 38	78.2	3.6	638	12	BJ461550
C 39	78	3.6	617	14	CA743799
C 40	77.8	3.6	223	13	CA022136
C 41	77.8	3.6	538	28	AZ825077
C 42	77.8	3.6	585	28	AZ564151
C 43	77.8	3.6	613	29	CE357285
C 44	77.6	3.6	504	29	CG354005
C 45	77.6	3.6	871	29	CG354013

ALIGNMENTS

RESULT 1	CAY16220/c	CAY16220	289 bp	mRNA	linear	EST 26-NOV-2002
LOCUS	wdk3c.pk024.122	wdk3c	Triticum aestivum	cdna	clone wdk3c.pk024.122	
DEFINITION	5' end mRNA sequence.					
ACCESSION	CAY16220					
VERSION	EST.					
KEYWORDS	Triticum aestivum (bread wheat)					
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
ORGANISM	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;					
REFERENCE	1 (bases 1 to 289)					
AUTHORS	Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,					
TITLE	Miao, G., Carabier, N. and Hanafey, M.K.					
JOURNAL	DuPont Wheat cDNA Sequence					
COMMENT	Unpublished (2002)					
	Contact: Scott V. Tingey					
	Crop Genetics					
	E. I. DuPont de Nemours and Company					
	1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA					
	Tel: 302-631-2602					
	Fax: 302-631-2607					
	Email: Scott.V.Tingey@USA.dupont.com					
	Seq primer: M13.					
	Location/Qualifiers					


```

RESULT 8
CA745444/c
LOCUS
DEFINITION
wri2s.pk001.i6 wri2s Triticum aestivum cDNA clone wri2s.pk001.i6 5'
end, mRNA sequence.
ACCESSION
CA745444
VERSION
CA745444.1 GI:25561267
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 434)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.tingey@USA.dupont.com
Seq primer: T7.
FEATURES
source
1..434
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wri2s.pk001.i6"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lib="wri2s"
/note="Vector: pGEM-T Easy; Site 1: SmaI; Riband
(susceptible) wheat leaves infected with Septoria tritici
strain A, 48 hours after infection, subtracted w/
comparable uninfected leaves"
ORIGIN
Query Match 3.7%; Score 81.4; DB 14; Length 434;
Best Local Similarity 64.0%; Pred. No. 2.9e-05;
Matches 121; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1349 AGGCGCAGGACGAGAGGATTCGGACATTGTAATGGCGAAGACGCGAATCG 1408
|||||
DB 360 AGGAGGACGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301
QY 1409 GCGNTGAGAGAGGACCGGAGATGCGCCGAGGAGATGAGCGGAGAGAGCG 1468
|||||
DB 300 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
QY 1469 AAGCCACAGAAACGAGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATCGT 1528
|||||
DB 240 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 1529 CGCGAGAG 1537
|||||
DB 180 AAGAAGAG 172

RESULT 9
CA607797/c
LOCUS
DEFINITION
wri1.pk0082.f4 wri1 Triticum aestivum cDNA clone wri1.pk0082.f4 5'
end, mRNA sequence.
ACCESSION
CA607797
VERSION
CA607797.1 GI:25162959
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 265)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.tingey@USA.dupont.com
Seq primer: M13.
FEATURES
source
1..265
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wri1.pk0082.f4"
/tissue_type="root"
/clone_lib="wri1"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) root; 7 day old
seedling, light grown"
ORIGIN
Query Match 3.7%; Score 81.2; DB 14; Length 265;
Best Local Similarity 64.1%; Pred. No. 3.1e-05;
Matches 116; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1357 GACGAGAGGATTCGGACATTGTAATGGCGAAGAGAGAGAGAGAGAGAGAG 1416
|||||
DB 184 GATGAGAGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125
QY 1417 GAAAGAGGACCGAGAGATGCGCGCAGGAGATGAGCGAGAGAGAGAGAGAGAG 1476
|||||
DB 124 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 65
QY 1477 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1536
|||||
DB 64 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5
QY 1537 G 1537
4 G 4
DB 4 G 4

RESULT 10
BH360392
LOCUS
DEFINITION
CH230-107G3.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-107G3, genomic survey sequence.
ACCESSION
BH360392
VERSION
BH360392.1 GI:17291126
KEYWORDS
GSS.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 719)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-107G3.TU
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

```

Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.choi.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ering information.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 107 row: G column: 3
 Seq primer: T7
 Class: BAC ends.

FEATURES

source

1. .719
 /location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-107G3"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 1"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 3.7%; Score 81.2; DB 28; Length 719;
 Best Local Similarity 61.2%; Pred. No. 3.2e-05;
 Matches 131; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1340 CCAACCGAAGGCGGAGGACGAGAGGATTCGGACATGTGATGCGAAGAGCGAAG 1399
 Db 229 CCCAAATGAAGGAGGAGGAGGATGAGGAGATGAAGCATGATGCGAAGAGG 288

QY 1400 ACCAAATCGCGATGAAGAGAGGACCGAAGATGCGCGGAGGAGATGAAGGACG 1459
 Db 289 AGAGAGGAG 348

QY 1460 AAGAAGACGAGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
 Db 349 AAGAAG 408

QY 1520 AAGAATCGTCGCGAGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1553
 Db 409 AAAAAGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 442

RESULT 11

BU005139/c
 LOCUS 263 bp mRNA linear EST 22-AUG-2002
 DEFINITION QG7D20.Y9.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
 QG7D20, mRNA sequence.
 ACCESSION BU005139
 VERSION BU005139.1 GI:22439534
 KEYWORDS EST.
 SOURCE Lactuca sativa
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Lactuca.
 1 (bases 1 to 263)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevallier, P., Ziegler, J.,
 Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
 Lai, Z., Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://compgenomics.ucdavis.edu/
 Unpublished (2002)
 CONTACT: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
 singleton, see http://cgdb.ucdavis.edu/ for details.
 Plate: QG7 row: D column: 20.

FEATURES

source

1. .263
 /location/Qualifiers
 /organism="Lactuca sativa"
 /mol_type="mRNA"
 /cultiivar="L.serriola"
 /db_xref="taxon:4236"
 /clone="QG7D20"
 /lab_host="E.coli"
 /clone_lib="QG_EFGHJ lettuce serriola"
 /note="Vector: pBRCN5FIAB; The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgdb.ucdavis.edu/
 TAG_SEQ=Not found"

ORIGIN

Query Match 3.7%; Score 81; DB 13; Length 263;
 Best Local Similarity 62.7%; Pred. No. 3.3e-05;
 Matches 126; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1343 AACCGAAGGCGGAGGACGAGGATTCGGACATGTGATGCGAAGAGCGAAGACG 1402
 Db 263 AACAGACAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 204

QY 1403 AAATCGCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1462
 Db 203 AAGAAG 144

QY 1463 AAGACGAGCCAG 1522
 Db 143 AAGAAG 84

QY 1523 AATCGTCGCGAGAGGAGGACG 1543
 Db 83 AAGACGAGAGAGAGAGAGAGAG 63

RESULT 12

CE180020
 LOCUS 729 bp DNA linear GSS 25-SEP-2003
 DEFINITION tigr-gss-dog-17000326768259 Dog Library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE180020
 VERSION CE180020.1 GI:35328914
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 729)
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432
 14512627
 PUBLISHED
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200

Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
Location/Qualifiers

1..729
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 3.7%; Score 80.8; DB 29; Length 729;
Best Local Similarity 61.3%; Pred. No. 3.8e-05;
Matches 130; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1342 AAACCGAGGCGCAGGACGAGGATTTCGGACATTGATAATGGCGAAGAAAGCGAAGAC 1401
DB 172 AAGAAGAA 231

QY 1402 GAAATCGGCGATGAAG 1461
DB 232 GAAGAAGAA 291

QY 1462 GAAGAA 1521
DB 292 GAAGAAGAA 351

QY 1522 GAATCGCGGAA 1553
DB 352 GAAGAATAGGATCAAAATATGATTTAAACA 383

RESULT 13

B0241566

LOCUS

DEFINITION BQ241566 264 bp mRNA linear EST 03-MAY-2002
TaE05003E07R Triticum aestivum cDNA clone TaE05003E07R, mRNA sequence.

ACCESSION

BQ241566

VERSION

BQ241566.1

GI:20437442

KEYWORDS

EST

SOURCE

Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

REFERENCE

1 (bases 1 to 264)

Cloutier, S.

Wheat functional genomics - Glenlea developing seeds cDNA libraries

Unpublished (2002)

Contact: Dr. Sylvie Cloutier

Cereal Research Centre, Agriculture and Agri-food Canada

195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9

Tel: (204) 983-2340

Fax: (204) 983-4604

Email: scloutier@agr.gc.ca

was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).

Average insert size is >2.0 kb

Plate: 003 row: E column: 07

Seq primer: M3 Reverse.

Location/Qualifiers

1..264

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Glenlea"

/db_xref="taxon:4565"

/clone="TaE05003E07R"

/tissue_type="developing seeds"

/dev_stage="5 days after anthesis"

/lab_host="E. coli DH10B"

FEATURES

source

Location/Qualifiers

1..264

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Glenlea"

/db_xref="taxon:4565"

/clone="TaE05003E07R"

/tissue_type="developing seeds"

/dev_stage="5 days after anthesis"

/lab_host="E. coli DH10B"

/clone_lib="TaE05"

/note="Vector: pSPORT-P (Invitrogen Technologies); Site 1: NotI; Site 2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis"

ORIGIN

Query Match 3.7%; Score 80.6; DB 13; Length 264;
Best Local Similarity 65.0%; Pred. No. 4e-05;
Matches 119; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1355 AGGACGAAGAGGATTTCGGACATTGATAATGGCGAAGAAAGCGAAGAAATCGGCGATG 1414
DB 49 AAGAAGAA 108

QY 1415 AAGAAGAA 1474
DB 109 AAGAAGAA 168

QY 1475 CAGAAAACGAAGCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1534
DB 169 AAGAAGAA 228

QY 1535 AAG 1537
DB 229 AAG 231

RESULT 14

B1504790

LOCUS

DEFINITION B1504790 501 bp mRNA linear EST 08-APR-2002
BBI70011A10D02.5 Bee Brain Normalized/Subtracted Library, BBI7 Apis mellifera cDNA clone BBI70011A10D02 5', mRNA sequence.

ACCESSION

B1504790

VERSION

B1504790.1

GI:15355164

KEYWORDS

EST.

SOURCE

Apis mellifera (honeybee)

ORGANISM

Apis mellifera

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.

REFERENCE

1 (bases 1 to 501)

Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,

Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.

Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee

Genome Res. 12 (4), 555-566 (2002)

21929762

PUBMED

11932240

COMMENT

Contact: Gene E. Robinson

Department of Entomology

University of Illinois

505 S. Goodwin Ave., Urbana, IL 61801, USA

Tel: 217 265 0309

Fax: 217 244 3499

Email: generobi@life.uiuc.edu

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Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation

Award in Functional Genomics to G.E. Robinson and an NSF

Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

REPEAT IN THE SEQUENCE

Simple repeat STRAND (+) ELEMENT (GAA)n LOCATION [67,246].

PCR Primers

FORWARD: TTAATACGACTCACTATAGG

BACKWARD: ATTAACTCTACTAAAG

Plate: BBI70011A10 row: D column: 02

Seq primer: AGCGGATACAAATTCACACAGGA

High quality sequence stop: 501.

FEATURES

source

Location/Qualifiers

1..501

/organism="Apis mellifera"

/mol_type="mRNA"

/strain="mixed strains of European bees, predominantly A.m. ligustica"

